

Substitute_Sequence_Listing.TXT

SEQUENCE LISTING

<110> Yoshinori Watanabe

<120> Novel centromeric protein SHUGOSHIN

<130> 4439-4043

<140> 10/581,158

<141> 2007-01-30

<150> JP2003-401943

<151> 2003-12-01

<150> JP2004-279450

<151> 2004-09-27

<160> 45

<170> PatentIn version 3.1

<210> 1

<211> 960

<212> DNA

<213> yeast

<400> 1

```

atgaactttc aatttataaa ttcaaataa aacaatgaag ataaattgcc gatggagtcg      60
ttgaaaaaga aattttttaa acaaaatcgt gaaattataa aaataaatac tcagctttct      120
ataaaaaatta gagaatctga aaacgaaatt caagatttga tacaagaaaa tttcactttg      180
aaaagttatt tggttaaact tgaagctcga tttcgcaatc aatctcaaac tgaggacttg      240
ttaaaaaact tctttcctga gatacaaacc attcacaaaa agatttcaca agtgcaaagt      300
ttactgaaga ttatagagaa aaagtgttca tcagatttcc tcgaagcgaa tgtaaaaaagt      360
caatttacia cctgtgaaaa taaagattcg aaagaagatt atcagatttt gcataataaa      420
cgcttggagt atgtatcatt taatgatgaa cttaaaagtc tcgaaacagg gcaaccattg      480
tattgttttc aagatttcca aaaaaaagtc catggtcctc cggctctatc tgaaaaacct      540
ggaaaatgta tattaagaaga taaaaccaat gccacgtaa aaaaataacc acaagatgag      600
gtgaattact cattgccgca aaaaaatatc accatctttt caaaggaatt aaaagaaaac      660
gaatttgaat ccatcaacga gggcgaaact gaagaagaaa aggctaaaac atcaaatggt      720
tgtgtttgta ttccttgtaa aagtgtctga cagataactg accttaaagg acaagcaacc      780
ggagacagct ccccatgtga ttttgaagaa tctcaaccaa ggattaatgg acgtgaaaaa      840
ctaagacgat cagtcaaagt gataaactat gcaataccca gtttgcgaaac taaactacga      900
cgagactttg acttaccatc tgatagaaaa cgcaaacgac atcccagagg caaagcataa      960

```

<210> 2

<211> 319

<212> PRT

Substitute_Sequence_Listing.TXT

<213> yeast

<400> 2

```

Met Asn Phe Gln Phe Ile Asn Ser Asn Ile Asn Asn Glu Asp Lys Leu
1      5      10
Pro Met Glu Ser Leu Lys Lys Lys Phe Leu Lys Gln Asn Arg Glu Ile
      20      25      30
Ile Lys Ile Asn Thr Gln Leu Ser Ile Lys Ile Arg Glu Ser Glu Asn
      35      40      45
Glu Ile Gln Asp Leu Ile Gln Glu Asn Phe Thr Leu Lys Ser Tyr Leu
      50      55      60
Val Lys Leu Glu Ala Arg Phe Arg Asn Gln Ser Gln Thr Glu Asp Leu
      65      70      75      80
Leu Lys Asn Phe Phe Pro Glu Ile Gln Thr Ile His Lys Lys Ile Ser
      85      90      95
Gln Val Gln Ser Leu Leu Lys Ile Ile Glu Lys Lys Cys Ser Ser Asp
      100      105      110
Phe Leu Glu Ala Asn Val Lys Ser Gln Phe Thr Thr Cys Glu Asn Lys
      115      120      125
Asp Ser Lys Glu Asp Tyr Gln Ile Leu His Asn Lys Arg Leu Glu Tyr
      130      135      140
Val Ser Phe Asn Asp Glu Leu Lys Ser Leu Glu Thr Gly Gln Pro Leu
      145      150      155      160
Tyr Cys Phe Gln Asp Phe Gln Lys Lys Val His Gly Pro Pro Ala Leu
      165      170      175
Ser Glu Lys Pro Gly Lys Cys Ile Leu Lys Asp Lys Thr Asn Ala His
      180      185      190
Val Asn Lys Ile Pro Gln Asp Glu Val Asn Tyr Ser Leu Pro Gln Lys
      195      200      205
Asn Ile Thr Ile Phe Ser Lys Glu Leu Lys Glu Asn Glu Phe Glu Ser
      210      215      220
Ile Asn Glu Gly Glu Thr Glu Glu Glu Lys Ala Lys Thr Ser Asn Val
      225      230      235      240

```

Substitute_Sequence_Listing.TXT

Cys Val Cys Ile Pro Cys Lys Ser Ala Glu Gln Ile Thr Asp Leu Lys
245 250 255

Gly Gln Ala Thr Gly Asp Ser Ser Pro Cys Asp Phe Glu Glu Ser Gln
260 265 270

Pro Arg Ile Asn Gly Arg Glu Lys Leu Arg Arg Ser Val Lys Val Ile
275 280 285

Asn Tyr Ala Ile Pro Ser Leu Arg Thr Lys Leu Arg Arg Asp Phe Asp
290 295 300

Leu Pro Ser Asp Arg Lys Arg Lys Arg His Pro Arg Gly Lys Ala
305 310 315

<210> 3
<211> 1944
<212> DNA
<213> yeast

<400> 3
atgtcgaag catctctttc cccgaacgta gaagacttga aaaaaagca aattcgacag 60
tataaggaaa ttatacgaat aagcaaggca caatcaatta gaattaaaga attgcagtta 120
gaaaatgaac ggttgctttc ggaaaatatc gatttgagga ctacagcgat aaacttggaa 180
gagcaactcg aaaccgtgca aaacgaaaac gaagaaaaca aaacaaagtt agctgcatta 240
cttaatcgat ttcatgaaga aacagataat tttttatcaa aattaagtct ttgtcagcaa 300
gaaatacaag acaccttcaa accagtggag gctaacttag cttacgatgt cgatacggat 360
tctgaagacc ttgacgagga atccgctcgtg aaagataccg aagaaataat tgagcaagct 420
cagcatgatg tttccttacg aaatttaagt ggaatagagg atgaaaatat aattgatgac 480
ggagaaaactg ctataaatga aaaaaaaaaa agagaagcta atgttttttc cgacacgcaa 540
tcagcacctc agctaaaatc cggcaaagcc ctcccagctg attttgaaaa tccttacaat 600
ctatccaatt cgaaacctgt aaataataat aatgaagata gagttgaagc ggttacttct 660
gaaaataaat ctatcgattc tgctcctcag gaaaaaaatc atgaatacga aatcgttagt 720
ccaaaatcat tatccaacaa aattaataat caagcagctg cacaagaag aaccgaagaa 780
gataatgcaa atggagttgc tcaagaagaa aatgaggggt cacaagaagc tcattttcat 840
agcagaatac aatctgatac agtaatacaa agtacacca ctaaacggaa atgggacgtt 900
gacattcaaa ataaacaaat taatctggct tctgcagcta ccaatgttac cggttatgta 960
tcggagaccg atagtcgccc caatcgcgca aactcttttg attctgctgt ccttcttggtg 1020
caatcttcaa ataaaagtaa ccgaaatggg catcatattt cagatcctaa tttaaatagc 1080

Substitute_Sequence_Listing.TXT

```
tccatatcgt tgaagtttgc gcctgaagat actgcgcata attcattaac ttcacaagag 1140
aatgttgggc ctcaggttac gacgacttct ctgtcaaata tgactgttgc tgaatctcct 1200
cgtacagaca ctccaagggg aataaacggg ttagtagact cttctgtcac taatgggaac 1260
gaaaaatttt ctgtagaaat aatgaatgac tctaacaaaa ttggactgaa tcctaaatct 1320
tttaccgacg aagagcggga aattttaaca ctttttcgaa atcctcccat gagactgtca 1380
agtgaacctc catcttcaaa tggattttca atagcccatc ccaataattc tccgttacgt 1440
ccgccatcgc tacaaggaat attgaatgct gaagatcgac cttacgaaat tgagccgtca 1500
cgtagctcct ttgctaccaa cgatacgggc tcctataata atttggaact tctgtcatct 1560
gtaacgaatt tgaaatcccc taatgagaac gatcgtgtga cgaaaactca gtcgcgaaga 1620
gaaacaaaag tgaaaaggcg aagaaaagct cggattcaag aaacttctga agaaagtaca 1680
gtagtcaatg agccaaatga aaaacctgat ggaaggagcc gaagggaacg gaaaaagggt 1740
aattacgctt tgcctggatt aaggacgaaa ttaagacgga atttcgattt accttcagat 1800
catgtaaaaag ctaaaaaaac gagacgtgct cctaagaact ctgagaatga ttcagctacc 1860
aaaacagaaa ccgcaaacat tacttctgaa gcaccacta cttcagaagt aacccttgaa 1920
aactccgaaa cccttaattt gtaa 1944
```

```
<210> 4
<211> 647
<212> PRT
<213> yeast
```

```
<400> 4
```

```
Met Ser Lys Ala Ser Leu Ser Pro Asn Val Glu Asp Leu Lys Lys Lys
1 5 10 15
```

```
Gln Ile Arg Gln Tyr Lys Glu Ile Ile Arg Ile Ser Lys Ala Gln Ser
20 25 30
```

```
Ile Arg Ile Lys Glu Leu Gln Leu Glu Asn Glu Arg Leu Leu Ser Glu
35 40 45
```

```
Asn Ile Asp Leu Arg Thr Thr Ala Ile Asn Leu Glu Glu Gln Leu Glu
50 55 60
```

```
Thr Val Gln Asn Glu Asn Glu Glu Asn Lys Thr Lys Leu Ala Ala Leu
65 70 75 80
```

```
Leu Asn Arg Phe His Glu Glu Thr Asp Asn Phe Leu Ser Lys Leu Ser
85 90 95
```

```
Leu Cys Gln Gln Glu Ile Gln Asp Thr Phe Lys Pro Val Glu Ala Asn
```

Substitute_Sequence_Listing.TXT

100																			
Leu	Ala	Tyr	Asp	Val	Asp	Thr	Asp	Ser	Glu	Asp	Leu	Asp	Glu	Glu	Ser				
		115					120					125							
Val	Val	Lys	Asp	Thr	Glu	Glu	Ile	Ile	Glu	Gln	Ala	Gln	His	Asp	Val				
	130					135					140								
Ser	Leu	Arg	Asn	Leu	Ser	Gly	Ile	Glu	Asp	Glu	Asn	Ile	Ile	Asp	Asp				
145					150					155					160				
Gly	Glu	Thr	Ala	Ile	Asn	Glu	Gln	Lys	Lys	Arg	Glu	Ala	Asn	Val	Phe				
				165					170					175					
Ser	Asp	Thr	Gln	Ser	Ala	Pro	Gln	Leu	Lys	Ser	Gly	Lys	Ala	Leu	Pro				
			180					185						190					
Ala	Asp	Phe	Glu	Asn	Pro	Tyr	Asn	Leu	Ser	Asn	Ser	Lys	Pro	Val	Asn				
		195					200					205							
Asn	Asn	Asn	Glu	Asp	Arg	Val	Glu	Ala	Val	Thr	Ser	Glu	Asn	Lys	Ser				
	210					215					220								
Ile	Asp	Ser	Ala	Pro	Gln	Glu	Lys	Asn	His	Glu	Tyr	Glu	Ile	Val	Ser				
225					230					235					240				
Pro	Lys	Ser	Leu	Ser	Asn	Lys	Ile	Asn	Asn	Gln	Ala	Ala	Ala	Gln	Arg				
				245					250					255					
Arg	Thr	Glu	Glu	Asp	Asn	Ala	Asn	Gly	Val	Ala	Gln	Glu	Glu	Asn	Glu				
			260					265					270						
Gly	Ser	Gln	Glu	Ala	His	Phe	His	Ser	Arg	Ile	Gln	Ser	Asp	Thr	Val				
		275					280					285							
Ile	Gln	Ser	Thr	Pro	Thr	Lys	Arg	Lys	Trp	Asp	Val	Asp	Ile	Gln	Asn				
	290					295					300								
Lys	Gln	Ile	Asn	Leu	Ala	Ser	Ala	Ala	Thr	Asn	Val	Thr	Gly	Tyr	Val				
305					310					315					320				
Ser	Glu	Thr	Asp	Ser	Arg	Pro	Asn	Arg	Ala	Asn	Ser	Leu	Asp	Ser	Ala				
				325					330					335					
Val	Leu	Leu	Val	Gln	Ser	Ser	Asn	Lys	Ser	Asn	Arg	Asn	Gly	His	His				
			340					345					350						

Substitute_Sequence_Listing.TXT

Ile Ser Asp Pro Asn Leu Asn Ser Ser Ile Ser Leu Lys Phe Ala Pro
355 360 365

Glu Asp Thr Ala His Asn Ser Leu Thr Ser Gln Glu Asn Val Gly Pro
370 375 380

Gln Val Thr Thr Thr Ser Leu Ser Asn Met Thr Val Ala Glu Ser Pro
385 390 395 400

Arg Thr Asp Thr Pro Arg Glu Ile Asn Gly Leu Val Asp Ser Ser Val
405 410 415

Thr Asn Gly Asn Glu Lys Phe Ser Val Glu Ile Met Asn Asp Ser Asn
420 425 430

Lys Ile Gly Leu Asn Pro Lys Ser Phe Thr Asp Glu Glu Arg Glu Ile
435 440 445

Leu Thr Leu Phe Arg Asn Pro Pro Met Arg Leu Ser Ser Glu Pro Pro
450 455 460

Ser Ser Asn Gly Phe Ser Ile Ala His Pro Asn Asn Ser Pro Leu Arg
465 470 475 480

Pro Pro Ser Leu Gln Gly Ile Leu Asn Ala Glu Asp Arg Pro Tyr Glu
485 490 495

Ile Glu Pro Ser Arg Ser Ser Phe Ala Thr Asn Asp Thr Gly Ser Tyr
500 505 510

Asn Asn Leu Glu Leu Leu Ser Ser Val Thr Asn Leu Lys Ser Pro Asn
515 520 525

Glu Asn Asp Arg Val Thr Lys Thr Gln Ser Arg Arg Glu Thr Lys Val
530 535 540

Lys Arg Arg Arg Lys Ala Arg Ile Gln Glu Thr Ser Glu Glu Ser Thr
545 550 555 560

Val Val Asn Glu Pro Asn Glu Lys Pro Asp Gly Arg Ser Arg Arg Glu
565 570 575

Arg Lys Lys Val Asn Tyr Ala Leu Pro Gly Leu Arg Thr Lys Leu Arg
580 585 590

Arg Asn Phe Asp Leu Pro Ser Asp His Val Lys Ala Lys Lys Thr Arg
595 600 605

Substitute_Sequence_Listing.TXT

Arg Ala Pro Lys Asn Ser Glu Asn Asp Ser Ala Thr Lys Thr Glu Thr
610 615 620

Ala Asn Ile Thr Ser Glu Ala Pro Thr Thr Ser Glu Val Thr Leu Glu
625 630 635 640

Asn Ser Glu Thr Leu Asn Leu
645

<210> 5
<211> 1773
<212> DNA
<213> yeast

```

<400> 5
atgccgaaga gaaaaattgc tcctaacaag gaaagcagca ggcgtacggt ctcccacgat      60
gatttaaccc cacaaatata agaatttcaa aacctaattg atctcgaatc gcaaaaagtg      120
gaaaacatca gacagtcgta ttcgaggcaa aactccctgc tggccaagga taactccata      180
ttaaaaaatta aagttaatat cttggaaaaa aaaataagcc agctggtaca agaaaacgtg      240
actctacgat ctaaaacctc tataagcgaa gctatctaca gggaacgggt aagtaatcaa      300
ctacaagtca ttgaaaacgg tattattcaa agatttgacg aaatttttta tatgtttgag      360
aacgtacgta aaaacgaaaa ttgtcccgat tcgagcttaa gaacaatggt gaagagaacg      420
agttccagggt caagatcatg ctcatgtgca tcaccacat actcaaaaag ttacactagg      480
ttatcaaatac acgagaataa cctgtcgcat gaatcaagtt ttaacaagga cgatggtcca      540
gatcttgagc ctaaggctaa aaaaaggaag agttctaggc ggcaatctat gtttgatatcc      600
acgagtttag aacctgaaga cgaaaccggt gaaaacgaac ccatgatgga aaattcctct      660
gtagaggtag cggcagaatc acacgagtct gcgcaagtgg aggaaacaat agatgcctta      720
aaccctgaag aggaaaatag cgattctgtc agtaatttta ccaattcaat tatagaatac      780
tccataccag aggagaatcc gacagaaccc gagcattcat cttctaaact agaaatattc      840
aatgacagta caaatatgct aagtacagtg ccgtaaatac ctttgccggt gcctttacca      900
ggcccatccg caactttacc tactaccact agcgatgctt caacgggtcta tccttcatca      960
agttcttcta ctaatttcta tccaaagacc aaaattaagc attccatgaa gccgcctagg     1020
atagaactga agaaaaaggt tattgacgaa gtcatgcccc taagtaacat gagcagcaac     1080
agcgaaatat catttacgag aactagaaga actcgtggta aagctgtaga ttacactttg     1140
ccttctttaa gagccaaat gaggaggcct tcagaaaaac ttgtggatgc tactactgtg     1200
attgatatac atgatctaca ggtttccaag agaaatcggg aaacttcaca taaaaggaaa     1260
agtttatccc aagattcaat acccgacgaa ccgcaattga gagaagtcgt cgtctcaaag     1320

```

Substitute_Sequence_Listing.TXT

```

gattatggaa ctccaaaagg gaaaaaaacg gaagatgaaa tacacgagga taccgctcat 1380
ctaatgacca cttccaacaa caacagcaac aacaaaaacg aaaaaaaact aactagcaac 1440
aatagcccta aaaaatcgtc gcctttactt gacattacaa ataaatcgga gaataagaaa 1500
aagtcaacaa gaactaaaaa attgttcaaa aatgcaattg tcaataattt atctgatgaa 1560
aattctacta cgcgaccctc caagtcgtca aagggaacca gtaataataa caacaattac 1620
aacaatttcg acaataacaa ttcaaacatt aataatgtta ataataaatc tgttagcttt 1680
agactaaatg aagatgattt agcagtattt gatttatttg gaaatggtaa ggcagtgttaa 1740
catcaaccaa aaacatatcg caccaaaaaa tga 1773

```

```

<210> 6
<211> 590
<212> PRT
<213> yeast

```

```

<400> 6

```

```

Met Pro Lys Arg Lys Ile Ala Pro Asn Lys Glu Ser Ser Arg Arg Thr
1      5      10     15

```

```

Val Ser His Asp Asp Leu Thr Pro Gln Ile Gln Glu Phe Gln Asn Leu
      20     25     30

```

```

Met Asp Leu Glu Ser Gln Lys Val Glu Asn Ile Arg Gln Ser Tyr Ser
      35     40     45

```

```

Arg Gln Asn Ser Leu Leu Ala Lys Asp Asn Ser Ile Leu Lys Ile Lys
      50     55     60

```

```

Val Asn Ser Leu Glu Lys Lys Ile Ser Gln Leu Val Gln Glu Asn Val
      65     70     75     80

```

```

Thr Leu Arg Ser Lys Thr Ser Ile Ser Glu Ala Ile Tyr Arg Glu Arg
      85     90     95

```

```

Leu Ser Asn Gln Leu Gln Val Ile Glu Asn Gly Ile Ile Gln Arg Phe
      100    105    110

```

```

Asp Glu Ile Phe Tyr Met Phe Glu Asn Val Arg Lys Asn Glu Asn Leu
      115    120    125

```

```

Pro Ser Ser Ser Leu Arg Thr Met Leu Lys Arg Thr Ser Ser Arg Ser
      130    135    140

```

```

Arg Ser Cys Ser Leu Ser Ser Pro Thr Tyr Ser Lys Ser Tyr Thr Arg
      145    150    155    160

```


Substitute_Sequence_Listing.TXT

Leu Ser Asn His Glu Asn Asn Leu Ser His Glu Ser Ser Phe Asn Lys
 165 170 175
 Asp Asp Gly Pro Asp Leu Glu Pro Lys Ala Lys Lys Arg Lys Ser Ser
 180 185 190
 Arg Arg Gln Ser Met Phe Val Ser Thr Ser Leu Glu Pro Glu Asp Glu
 195 200 205
 Thr Gly Glu Asn Glu Pro Met Met Glu Asn Ser Ser Val Glu Val Pro
 210 215 220
 Ala Glu Ser His Glu Ser Ala Gln Val Glu Glu Thr Ile Asp Ala Leu
 225 230 235 240
 Asn Pro Glu Glu Glu Asn Ser Asp Ser Val Ser Asn Phe Thr Asn Ser
 245 250 255
 Ile Ile Glu Tyr Ser Ile Pro Glu Glu Asn Pro Thr Glu Pro Glu His
 260 265 270
 Ser Ser Ser Lys Leu Glu Ile Phe Asn Asp Ser Thr Asn Met Leu Ser
 275 280 285
 Thr Val Pro Ser Asn Pro Leu Pro Leu Pro Leu Pro Gly Pro Ser Ala
 290 295 300
 Thr Leu Pro Thr Thr Thr Ser Asp Ala Ser Thr Val Tyr Pro Ser Ser
 305 310 315 320
 Ser Ser Ser Thr Asn Ser His Pro Lys Thr Lys Ile Lys His Ser Met
 325 330 335
 Lys Pro Pro Arg Ile Glu Leu Lys Lys Lys Val Ile Asp Glu Val Met
 340 345 350
 Pro Val Ser Asn Met Ser Ser Asn Ser Glu Ile Ser Phe Thr Arg Thr
 355 360 365
 Arg Arg Thr Arg Gly Lys Ala Val Asp Tyr Thr Leu Pro Ser Leu Arg
 370 375 380
 Ala Lys Met Arg Arg Pro Ser Glu Lys Leu Val Asp Ala Thr Thr Val
 385 390 395 400
 Ile Asp Ile His Asp Leu Gln Val Ser Lys Arg Asn Arg Glu Thr Ser
 405 410 415

Substitute_Sequence_Listing.TXT

His Lys Arg Lys Ser Leu Ser Gln Asp Ser Ile Pro Asp Glu Pro Gln
420 425 430

Leu Arg Glu Val Val Val Ser Lys Asp Tyr Gly Thr Pro Lys Gly Lys
435 440 445

Lys Thr Glu Asp Glu Ile His Glu Asp Thr Ala His Leu Met Thr Thr
450 455 460

Ser Asn Asn Asn Ser Asn Asn Lys Asn Glu Lys Lys Leu Thr Ser Asn
465 470 475 480

Asn Ser Pro Lys Lys Ser Ser Pro Leu Leu Asp Ile Thr Asn Lys Ser
485 490 495

Glu Asn Lys Lys Lys Ser Thr Arg Thr Lys Lys Leu Phe Lys Asn Ala
500 505 510

Ile Val Asn Asn Leu Ser Asp Glu Asn Ser Thr Thr Arg Pro Ser Lys
515 520 525

Ser Ser Lys Gly Thr Ser Asn Asn Asn Asn Asn Tyr Asn Asn Phe Asp
530 535 540

Asn Asn Asn Ser Asn Ile Asn Asn Val Asn Asn Lys Ser Val Ser Phe
545 550 555 560

Arg Leu Asn Glu Asp Asp Leu Ala Val Phe Asp Leu Phe Gly Asn Gly
565 570 575

Lys Ala Val Lys His Gln Pro Lys Thr Tyr Arg Thr Lys Lys
580 585 590

<210> 7
<211> 2325
<212> DNA
<213> Neurospora crassa

<400> 7	
atggccccgcc tcaacgaaca agccatgtcg tctgtcgcgt tgtcaacaga caatctcgag	60
ctcctgcgta ggaagttcct cagacaaaac agagatattg ctcgagtcaa ttccacacag	120
tcactccgta tccgtggggtt ggagaatgaa tgcgctcggt tgctgtcgga aaacctcgaa	180
ctccgtgggtc aggtcttgcg cctcgaaaag gagctccaag acaacgctgc gcgaaggggtg	240
gccgatcatg cgctcgaggt caaggccaag atggagacgc agttggcgga actcagttcg	300
ctgctggcaa gcttagggga gccgccctcg aagcggcgcc tttcagaaga gaggcgatac	360

Substitute_Sequence_Listing.TXT

gcgcagcctc	gaccgagcgt	tcaccggagc	cctcccttac	gaagagcacg	ccaggaggcc	420
gaccaggaac	tactggctga	gcaggaagga	aggctaccgc	cgatatacga	gaacaagacg	480
tatgcgcgag	ccacaatgaa	cagtgaagaa	atcctggcgc	tgtgcatgca	ggcagacgat	540
tcgaatgact	cgccagatat	cggaccgccg	ccagtatcta	ggtttgtcga	ggatgatatg	600
gtcatacctt	gttcaccatc	gccaaacaag	aacgccgagg	ctgaagaaac	ggaaactacc	660
gagcaagtgg	aagagagccc	tagggctctt	caagtaccgc	cgtcattatc	gccgcctaaa	720
ctggactacg	acaggagacc	aaacatgata	ctattcagcc	cacccaaaga	atcgagagtg	780
gcagaaccct	ccaaaatggt	cagtccccct	ccgatggaac	caccgaaaca	gtccacatcg	840
gctgtaccga	gtgagacaat	acgagcaggc	ctcaagcgaa	agttgaacgg	cgacaaccaa	900
aacgaacca	acaaggcaac	caagcttcaa	caaggaaagg	agaatggcaa	tgagactggg	960
atcaagaaa	gactctctgc	ccgcgacccg	cacaagagga	aaagcatcaa	agagaccgca	1020
acgaaaccga	gagccccgct	gtcagcaaag	agcacgaacg	agcacattgt	ctctccgaag	1080
aagccggcga	agccccacca	agtggccgac	gatttttaagc	cgggtgaagg	gcacaaggcg	1140
tcaaagggta	aagagaaagt	cgacctgccc	gctccggaca	agaagtcagc	agtagaagaa	1200
acgcaaggaa	attctacgtc	ggcattcacg	aaagtcgaga	tcctcccgcc	ggctctggaa	1260
cctactcctg	aagttgcaga	gattcctgaa	accgatattc	tgatcacacc	tggaacacca	1320
gagcgcgcct	ctgaaagcac	tgttgtgacc	cacgataccc	cgccgccagc	ccacatttca	1380
tccaatggag	agacgtcgcg	gcctagcagg	cggtgctagag	cggctatcag	ctatacagag	1440
cccaatctgc	gcgacaagat	gcgacgaccg	accaaagagc	tctttgatgc	cgtttctggg	1500
gagggcaagt	tcctacacag	gccgacatcg	caacagcaac	agcagcaacg	caagggcgac	1560
gagtcagcac	cgacgtcagt	tagcaaggtc	aaggtcgagc	catcgccggc	ggtggatata	1620
agtagtctga	ccagcagtgc	gctgtttgaa	aaagagaagg	agaaggaacc	acagccggat	1680
gaaggaatat	tatctccaaa	cggcatcctc	ccaagctcag	tagacctggg	aaggagaaga	1740
cgcgccctcat	ccttctctac	tgacgcccct	gcaatgacaa	ttccttcggt	ccaagaacaa	1800
tcaactctaa	acctcccagc	cgcggacgag	accgatgaaa	acgccgcggt	cgaggctcag	1860
attcagaagg	agctgagtaa	tagtattaca	acacggccca	ggggtggaaa	ggggaggcaa	1920
tcaatgagcc	gttccgtacc	cacgatccca	acagaaaatt	acgagcacga	ggacgcacaa	1980
ctctcgacga	actcagcctc	ggtggatctt	tacgactttg	ctagttgtgc	gtctccggat	2040
agcgcagcac	cccagctaga	agcgactacc	ggcgatgttc	ctgttaataa	gaaggcaccc	2100
aaagggttcaa	gaagagcgtc	ctcagctgct	tcgaccgaga	caacagcaac	agcatccgca	2160
aagccaagat	cttcccga	aagggttcg	atgctggtgc	cgaagaaaag	cttgtgggct	2220

Substitute_Sequence_Listing.TXT

gaagagttag cgcaggagga agaggatgag gaagatgtcg gcaatgacag tggcgggtcc 2280

ttgtccaagg ggagggcctc gaggaggaga agcatgatgc ttgga 2325

<210> 8

<211> 774

<212> PRT

<213> Neurospora crassa

<400> 8

Met Ala Arg Leu Asn Glu Gln Ala Met Ser Ser Val Ala Leu Ser Thr
1 5 10 15

Asp Asn Leu Glu Leu Leu Arg Arg Lys Phe Leu Arg Gln Asn Arg Asp
20 25 30

Ile Ala Arg Val Asn Ser Thr Gln Ser Leu Arg Ile Arg Gly Leu Glu
35 40 45

Asn Glu Cys Ala Arg Leu Leu Ser Glu Asn Leu Glu Leu Arg Gly Gln
50 55 60

Val Leu Arg Leu Glu Lys Glu Leu Gln Asp Asn Ala Ala Arg Arg Val
65 70 75 80

Ala Asp His Ala Leu Glu Val Lys Ala Lys Met Glu Thr Gln Leu Ala
85 90 95

Glu Leu Ser Ser Leu Leu Ala Ser Leu Gly Glu Pro Pro Ser Lys Arg
100 105 110

Arg Leu Ser Glu Glu Arg Arg Tyr Ala Gln Pro Arg Pro Ser Val His
115 120 125

Arg Ser Pro Pro Leu Arg Arg Ala Arg Gln Glu Ala Asp Gln Glu Leu
130 135 140

Leu Ala Glu Gln Glu Gly Arg Leu Pro Pro Ile Tyr Glu Asn Lys Thr
145 150 155 160

Tyr Ala Arg Ala Thr Met Asn Ser Glu Glu Ile Leu Ala Leu Cys Met
165 170 175

Gln Ala Asp Asp Ser Asn Asp Ser Pro Asp Ile Gly Pro Pro Pro Val
180 185 190

Ser Arg Phe Val Glu Asp Asp Met Val Ile Pro Cys Ser Pro Ser Pro
195 200 205

Substitute_Sequence_Listing.TXT

Asn Lys Asn Ala Glu Ala Glu Glu Thr Glu Thr Thr Glu Gln Val Glu
 210 215 220
 Glu Ser Pro Arg Ala Leu Gln Val Pro Pro Ser Leu Ser Pro Pro Lys
 225 230 235 240
 Leu Asp Tyr Asp Arg Arg Pro Asn Met Ile Leu Phe Ser Pro Pro Lys
 245 250 255
 Glu Ser Arg Val Ala Glu Pro Ser Lys Met Phe Ser Pro Pro Pro Met
 260 265 270
 Glu Pro Pro Lys Gln Ser Thr Ser Ala Val Pro Ser Glu Thr Ile Arg
 275 280 285
 Ala Gly Leu Lys Arg Lys Leu Asn Gly Asp Asn Gln Asn Glu Pro Asn
 290 295 300
 Lys Ala Thr Lys Leu Gln Gln Gly Lys Glu Asn Gly Asn Glu Thr Gly
 305 310 315 320
 Ile Lys Lys Gly Leu Ser Ala Arg Asp Pro His Lys Arg Lys Ser Ile
 325 330 335
 Lys Glu Thr Ala Thr Lys Pro Arg Ala Pro Leu Ser Ala Lys Ser Thr
 340 345 350
 Asn Glu His Ile Val Ser Pro Lys Lys Pro Ala Lys Pro His Gln Val
 355 360 365
 Ala Asp Asp Phe Lys Pro Val Lys Val His Lys Ala Ser Lys Gly Lys
 370 375 380
 Glu Lys Val Asp Leu Pro Ala Pro Asp Lys Lys Ser Ala Val Glu Glu
 385 390 395 400
 Thr Gln Gly Asn Ser Thr Ser Ala Phe Thr Lys Val Glu Ile Leu Pro
 405 410 415
 Pro Ala Leu Glu Pro Thr Pro Glu Val Ala Glu Ile Pro Glu Thr Asp
 420 425 430
 Ile Leu Ile Thr Pro Gly Thr Pro Glu Arg Ala Ser Glu Ser Thr Val

Substitute_Sequence_Listing.TXT

435
 Val Thr His Asp Thr Pro Pro Pro Ala His Ile Ser Ser Asn Gly Glu
 450 455 460
 Thr Ser Arg Pro Ser Arg Arg Ala Arg Ala Ala Ile Ser Tyr Thr Glu
 465 470 475 480
 Pro Asn Leu Arg Asp Lys Met Arg Arg Pro Thr Lys Glu Leu Phe Asp
 485 490 495
 Ala Val Ser Gly Glu Gly Lys Phe Leu His Arg Pro Thr Ser Gln Gln
 500 505 510
 Gln Gln Gln Gln Arg Lys Gly Asp Glu Ser Ala Pro Thr Ser Val Ser
 515 520 525
 Lys Val Lys Val Glu Pro Ser Pro Ala Val Asp Ile Ser Ser Leu Thr
 530 535 540
 Ser Ser Ala Leu Phe Glu Lys Glu Lys Glu Lys Glu Pro Gln Pro Asp
 545 550 555 560
 Glu Gly Ile Leu Ser Pro Asn Gly Ile Leu Pro Ser Ser Val Asp Leu
 565 570 575
 Gly Arg Arg Arg Arg Ala Ser Ser Phe Ser Thr Ala Ala Pro Ala Met
 580 585 590
 Thr Ile Pro Ser Val Gln Glu Gln Ser Thr Leu Asn Leu Pro Ala Ala
 595 600 605
 Asp Glu Thr Asp Glu Asn Ala Ala Val Glu Ala Gln Ile Gln Lys Glu
 610 615 620
 Leu Ser Asn Ser Ile Thr Thr Arg Pro Arg Gly Gly Lys Gly Arg Gln
 625 630 635 640
 Ser Met Ser Arg Ser Val Pro Thr Ile Pro Thr Glu Asn Tyr Glu His
 645 650 655
 Glu Asp Ala Gln Leu Ser Thr Asn Ser Ala Ser Val Asp Leu Tyr Asp
 660 665 670
 Phe Ala Ser Cys Ala Ser Pro Asp Ser Ala Ala Pro Gln Leu Glu Ala
 675 680 685

Substitute_Sequence_Listing.TXT

Thr Thr Gly Asp Val Pro Val Asn Lys Lys Ala Pro Lys Gly Ser Arg
690 695 700

Arg Ala Ser Ser Ala Ala Ser Thr Glu Thr Thr Ala Thr Ala Ser Ala
705 710 715 720

Lys Pro Arg Ser Ser Arg Lys Arg Ala Ser Met Leu Val Pro Lys Lys
725 730 735

Ser Leu Trp Ala Glu Glu Leu Ala Gln Glu Glu Glu Asp Glu Glu Asp
740 745 750

Val Gly Asn Asp Ser Gly Gly Ser Leu Ser Lys Gly Arg Ala Ser Arg
755 760 765

Arg Arg Ser Met Met Leu
770

<210> 9
<211> 1671
<212> DNA
<213> Arabidopsis thaliana

<400> 9
atggttcgag cgacggttct gaatgtcggg gatcacgcca gtgaaggtgt gcgtactaac 60
aaagctaaag gagagaaaat ggttctggaa cctccgatga acagtgcaca aagacgaaag 120
ttgggggata ttactaatTT gcagaatcag aagaatctaa tgaatcaggg agcgaagcat 180
cagcaacaag ctatattaat ctcttctaaa gaaaacgctg aaaatcttca aaaggcactg 240
agaaattctt ctgaaaacac aaagctgatg aaagtcgtca tggagagaga tggaatcaaa 300
agtgatctga agaaacttag gattgaattt cagaaggttc aagaacagaa tttgctactt 360
gcccaggcta acactcgtat cttggcgctg aagggtacttc agcacgaact tggttgcaag 420
aatggggttag tcatggccag gaaaatgctg ctttaaggctc aagcaaattgc ttgtggtggg 480
gcttgcaaaa cttttcagcc aaatgatgca gatcatgagc atgcttccgg gagctccaac 540
gctaactcat tgcaaagaaa tgagaaagcc aacagtataa ggagagtttc tggaaggaag 600
aatcccgcca attccgaggt attagatata attggcagat cgggagagac atgtcagatg 660
gaagacaaca ttgacaacaa gaagttgggtc tctgatagtg acaatgatgc tgaaaaccat 720
ataaatgaca atgtccaaag caaaagatat tgtgcaggaa gacagagtag cagttctaag 780
actcgagaag ccagccaaac agaaaccttg caaaagggtg ttgacgcaa agaaattaag 840
ggggatgcaa ggttttcttt gacaaagcat tctgactggg taaaatctca agaacctgag 900

Substitute_Sequence_Listing.TXT

```

ccatctgaaa gcctatacga gtcaagggtc cctttgagaa ggcgttctgc ccgggttaaaa    960
tctcaagaac ctgagccatc tgaaagcttc catgactcaa tagagacaac caagaggagg    1020

aggtcggcaa taaggtctgc tatgtttaat atccaagagc tgggcgttat tcaaaacttg    1080
aacggtttac ctgatgatca agagattgct gcaaaggcca gatgctctgc acgtgaacag    1140
tctaccgggt ctaaaccgga agcagtagaa ccacatgaca caaaagagat aatcgggaaa    1200
agcaggatat ctttgagaag acagtctgcg aggtttaatt tccaagagct gggcgtgact    1260
gaaaacttga atggtccaca tgatgatcaa acgattgctg caaatgccag atgctgtgca    1320
agtgaacagt ctatcgggtc taaaccgaa gcagtagaac cacatgacat tgaagagaga    1380
atcgggaaaa tcagagtctc ttcaagaaga caatctgcaa acattgaaac tccgagagcc    1440
atcaaagaac ctgcaaatcc gcctttgcat gatgacaatg ttgaggagtc tagtcagata    1500
tcatgttcag tttcaatgga gcttaaaaga gaatcaaaga agaaaccaac aggcgacgaa    1560
tcagaggaaa tgagaaaaac aactgttgga agaccttcaa ggcaagctgc tgaaaaaatc    1620
aaatcgtaca aggaaccttc acttaaggag aagatgagag ggggcttctg a          1671

```

```

<210> 10
<211> 556
<212> PRT
<213> Arabidopsis thaliana

<400> 10

```

```

Met Val Arg Ala Thr Val Leu Asn Val Gly Asp His Ala Ser Glu Gly
1          5          10          15

```

```

Val Arg Thr Asn Lys Ala Lys Gly Glu Lys Met Val Leu Glu Pro Pro
          20          25          30

```

```

Met Asn Ser Ala Gln Arg Arg Lys Leu Gly Asp Ile Thr Asn Leu Gln
          35          40          45

```

```

Asn Gln Lys Asn Leu Met Asn Gln Gly Ala Lys His Gln Gln Gln Ala
          50          55          60

```

```

Ile Leu Ile Ser Ser Lys Glu Asn Ala Glu Asn Leu Gln Lys Ala Leu
65          70          75          80

```

```

Arg Asn Ser Ser Glu Asn Thr Lys Leu Met Lys Val Val Met Glu Arg
          85          90          95

```

```

Asp Gly Ile Lys Ser Asp Leu Lys Lys Leu Arg Ile Glu Phe Gln Lys
          100          105          110

```


Substitute_Sequence_Listing.TXT

Val Gln Glu Gln Asn Leu Leu Leu Ala Gln Ala Asn Thr Arg Ile Leu
115 120 125

Ala Leu Lys Val Leu Gln His Glu Leu Gly Cys Lys Asn Gly Leu Val
130 135 140

Met Ala Arg Lys Met Leu Leu Lys Ala Gln Ala Asn Ala Cys Gly Gly
145 150 155 160

Ala Cys Lys Thr Phe Gln Pro Asn Asp Ala Asp His Glu His Ala Ser
165 170 175

Gly Ser Ser Asn Ala Asn Ser Leu Gln Arg Asn Glu Lys Ala Asn Ser
180 185 190

Lys Arg Arg Val Ser Gly Arg Lys Asn Pro Ala Asn Ser Glu Val Leu
195 200 205

Asp Ile Ile Gly Arg Ser Gly Glu Thr Cys Gln Met Glu Asp Asn Ile
210 215 220

Asp Asn Lys Lys Leu Val Ser Asp Ser Asp Asn Asp Ala Glu Asn His
225 230 235 240

Ile Asn Asp Asn Val Gln Ser Lys Arg Tyr Cys Ala Gly Arg Gln Ser
245 250 255

Ser Ser Ser Lys Thr Arg Glu Ala Ser Gln Thr Glu Thr Leu Gln Lys
260 265 270

Val Val Asp Ala Lys Glu Ile Lys Gly Asp Ala Arg Phe Ser Leu Thr
275 280 285

Lys His Ser Asp Trp Leu Lys Ser Gln Glu Pro Glu Pro Ser Glu Ser
290 295 300

Leu Tyr Glu Ser Arg Phe Pro Leu Arg Arg Arg Ser Ala Arg Leu Lys
305 310 315 320

Ser Gln Glu Pro Glu Pro Ser Glu Ser Phe His Asp Ser Ile Glu Thr
325 330 335

Thr Lys Arg Arg Ser Ala Ile Arg Ser Ala Met Phe Asn Ile Gln
340 345 350

Substitute_Sequence_Listing.TXT

Glu Leu Gly Val Ile Gln Asn Leu Asn Gly Leu Pro Asp Asp Gln Glu
355 360 365

Ile Ala Ala Lys Ala Arg Cys Ser Ala Arg Glu Gln Ser Thr Gly Ser
370 375 380

Lys Pro Glu Ala Val Glu Pro His Asp Thr Lys Glu Ile Ile Gly Lys
385 390 395 400

Ser Arg Ile Ser Leu Arg Arg Gln Ser Ala Arg Phe Asn Phe Gln Glu
405 410 415

Leu Gly Val Thr Glu Asn Leu Asn Gly Pro His Asp Asp Gln Thr Ile
420 425 430

Ala Ala Asn Ala Arg Cys Cys Ala Ser Glu Gln Ser Ile Gly Ser Lys
435 440 445

Pro Glu Ala Val Glu Pro His Asp Ile Glu Glu Arg Ile Gly Lys Ile
450 455 460

Arg Val Ser Ser Arg Arg Gln Ser Ala Asn Ile Glu Thr Pro Arg Ala
465 470 475 480

Ile Lys Glu Pro Ala Asn Pro Pro Leu His Asp Asp Asn Val Glu Glu
485 490 495

Ser Ser Gln Ile Ser Cys Ser Val Ser Met Glu Leu Lys Arg Glu Ser
500 505 510

Lys Lys Lys Pro Thr Gly Asp Glu Ser Glu Glu Met Arg Lys Thr Thr
515 520 525

Val Gly Arg Pro Ser Arg Gln Ala Ala Glu Lys Ile Lys Ser Tyr Lys
530 535 540

Glu Pro Ser Leu Lys Glu Lys Met Arg Gly Gly Phe
545 550 555

<210> 11
<211> 1341

<212> DNA
<213> Arabidopsis thaliana

<400> 11
atggataaag aagagacgca gcagaaggaa aatatgctat tctcttccca ggaatatgct 60
gcaaagcttc aaaaggcatt tcctcttcac tttaatcttg aaaacatgac actgatgaaa 120

Substitute_Sequence_Listing.TXT

```

gctctagcac accgaaataa actcgtcgag ttgagcggta ttgagattca gaaactgagg 180
attaacttac ggagtgtgca ggaaaagaat ttgcagcttg ctcaggcaaa cagtcagatg 240
ttagcgctca aggatctcca gcatgaactt ggctgcaaga atgctttact taaagtcaag 300
aaacatcttg aggagcaagt acttccacgt acacatcatg aatcgaaaga caagggttca 360
gcaagcgctt ctgatgggga ttgcaaatcc tttcaggtgc atgacataaa acataaagat 420
accaagagaa agcgaacaac aaggataaaa tcttcagtaa gtgccgacgt caagccaata 480
cctgtgaatg attctaacag taaagctaac cgtaaaagaa gagtttcttg agtaatagat 540
actactggta ttcccgaaga gatctgtcag actgaagatg acattgataa gggggttgtc 600
tctcgagggg taaaccaaga tattgacaat gttgtcaaca agaagtttgt tcctgatgca 660
gcaaaccggg taaaagagag tgtgcatcgc aagaggcaat gtacacgaag gcaatctacc 720
agatttgatg ttcaagaaac taaacaaacg gaaaagttgc ttgagatgga tggtgccaaa 780
gaaagtaaag aaaccgcaag cttctctttg agaagacggt ctgctcggtt aaggcacgaa 840
gaagctgaac catgtaaaag cttacatgag ggagacgaag tcaggagagac aatcaagagg 900
agaagagtct ctttaagact gtctgcaagg tttgatatac aagaaccgca tgtgactgaa 960
acctcgaatg ctgacgatgc aagaagcata gtaatcgaag aatctgctgg atcaagatcg 1020
gaatctgtag aaccatccga aagcaggcat gaaacaaaag agataaccg gaaacgcagt 1080
ttctcaacga gaagacaatc aacaaagggg aaatctcaaa ccgatgaagc cattaagaa 1140
atagcgacag acccatcttt ggtcaacacc atagttcaag agtgtgatca ggaaacagaa 1200
tcaaaggata agcctaaagc tgatgaaaac gaagggatga caagaagatc atctgtggga 1260
agaccatcga gacatgccgc agagaaagtc caatcataca gagaagtctc acttagagta 1320
aagatgcgac gaaaatgcta a 1341

```

```

<210> 12
<211> 446
<212> PRT
<213> Arabidopsis thaliana

```

<400> 12

```

Met Asp Lys Glu Glu Thr Gln Gln Lys Glu Asn Met Leu Phe Ser Ser
1          5          10          15

```

```

Gln Glu Tyr Ala Ala Lys Leu Gln Lys Ala Phe Pro Leu His Phe Asn
          20          25          30

```

```

Leu Glu Asn Met Thr Leu Met Lys Ala Leu Ala His Arg Asn Lys Leu
          35          40          45

```

Substitute_Sequence_Listing.TXT

Val Glu Leu Ser Gly Ile Glu Ile Gln Lys Leu Arg Ile Asn Leu Arg
50 55 60

Ser Val Gln Glu Lys Asn Leu Gln Leu Ala Gln Ala Asn Ser Gln Met
65 70 75 80

Leu Ala Leu Lys Asp Leu Gln His Glu Leu Gly Cys Lys Asn Ala Leu
85 90 95

Leu Lys Val Lys Lys His Leu Glu Glu Gln Val Leu Pro Arg Thr His
100 105 110

His Glu Ser Lys Asp Lys Val Ser Ala Ser Ala Ser Asp Gly Asp Cys
115 120 125

Lys Ser Phe Gln Val His Asp Ile Lys His Lys Asp Thr Lys Arg Lys
130 135 140

Arg Thr Thr Arg Ile Lys Ser Ser Val Ser Ala Asp Val Lys Pro Ile
145 150 155 160

Pro Val Asn Asp Ser Asn Ser Lys Ala Asn Arg Lys Arg Arg Val Ser
165 170 175

Gly Val Ile Asp Thr Thr Gly Ile Pro Glu Glu Ile Cys Gln Thr Glu
180 185 190

Asp Asp Ile Asp Lys Gly Val Val Ser Arg Gly Val Asn Gln Asp Ile
195 200 205

Asp Asn Val Val Asn Lys Lys Phe Val Pro Asp Ala Ala Asn Pro Val
210 215 220

Lys Glu Ser Val His Arg Lys Arg Gln Cys Thr Arg Arg Gln Ser Thr
225 230 235 240

Arg Phe Asp Val Gln Glu Thr Lys Gln Thr Glu Lys Leu Leu Glu Met
245 250 255

Asp Gly Ala Lys Glu Ser Lys Glu Thr Ala Ser Phe Ser Leu Arg Arg
260 265 270

Arg Ser Ala Arg Leu Arg His Glu Glu Ala Glu Pro Cys Lys Ser Leu
275 280 285

His Glu Gly Asp Glu Val Arg Glu Thr Ile Lys Arg Arg Arg Val Ser
290 295 300

Substitute_Sequence_Listing.TXT

Leu Arg Leu Ser Ala Arg Phe Asp Ile Gln Glu Pro His Val Thr Glu
305 310 315 320

Thr Ser Asn Ala Asp Asp Ala Arg Ser Ile Val Ile Glu Glu Ser Ala
325 330 335

Gly Ser Arg Ser Glu Ser Val Glu Pro Ser Glu Ser Arg His Glu Thr
340 345 350

Lys Glu Ile Thr Arg Lys Arg Ser Phe Ser Thr Arg Arg Gln Ser Thr
355 360 365

Lys Gly Lys Ser Gln Thr Asp Glu Ala Ile Lys Glu Ile Ala Thr Asp
370 375 380

Pro Ser Leu Val Asn Thr Ile Val Gln Glu Cys Asp Gln Glu Thr Glu
385 390 395 400

Ser Lys Asp Lys Pro Lys Ala Asp Glu Asn Glu Gly Met Thr Arg Arg
405 410 415

Ser Ser Val Gly Arg Pro Ser Arg His Ala Ala Glu Lys Val Gln Ser
420 425 430

Tyr Arg Glu Val Ser Leu Arg Val Lys Met Arg Arg Lys Cys
435 440 445

<210> 13
<211> 1554
<212> DNA
<213> mouse

<400> 13
atggcctaagg aaaggtgtca gaaaagggtcc tttcaagata cccttgaaga cattaagaat 60
cgaatgaaag aaaaaaggaa taaaaatttg gcggggattg ggaaacgcaa gtcctttatt 120
gttgccaccg gccaaagtacc cactaacact gctacactac tgagatatta ccaagataac 180
aacaggttgt tagtcttggc tttggaaaat gagaaatcca aagtgagaga agcacaggat 240
gtcatcctgc aactgagaaa agaattgctac taccttactt gtcagctgta tgcattgaaa 300

gagaagctaa cttcccgaca aagtgaagaa actactcaga actggaaagg acgtccctca 360
gacgtggtct ccagcattga caatacgacc agggacttgt cagggaagtc cttacagcaa 420
attgctgttg aagaaactga ttgtccttac caaaccacag aaccaagtcc tgctgttact 480
ccagagacac agggttgcga ttttgattca ggtaaagttg agtctactga tgaagtctta 540
cccagaacta tatctatccg tcgccattta aggaaagatt ttagtaatat aagccactcc 600

Substitute_Sequence_Listing.TXT

```

acgacttttg aggattgtaa agccagtcca agagtggcac agtctctgga agttaaagga 660
agtagatgta gagaagtaac cgtaaccctg cacagacttg aaaatgtttg tctgtggaac 720
aaagaccaaa ttagcttatg ttctagactg attaaccag caaagattac tgaaacagaa 780
gtcattttat catctaaacc tgaacaaata gaaagcaagc ataaacgtgc acgaaaaaga 840
agagcagagc aaagaagaac caagcagaga tgcaaatcaa aatcctcatt gaggagtaag 900
gggaacaaaa acaaagataa gcaggggtta cccctacta cactggatgg aggtattggt 960
tcctgtgatg cttacgattt taatctaaaa gggacggtcc accccacccc tttccgacaa 1020
aaaatgaaca atggctgcaa caaagaaacg gatagcagca actcagaagt gagtgcctc 1080
gaatgcagta cctctgagga tgagtctgat gacctctacc tgcctccctc caagcgcttg 1140
cgagactaca gagagtcaga gagagcagtt accaggcctc ggtctaaaag aggacttcag 1200
taccagatg ggaaagagag gaaggagggtg ctgccatcta cagctcctac tggtatccca 1260
cctgagactc aagagtcacc tcgttgtagc ctaaaggatg tcaccaatat cctgcagtgt 1320
cctagagtga agatcaggaa gccttctctg cctccaaagc ggcgtgaaga cagcccagca 1380
gtggctctga ctaaacgcag gtgtagcacc atcaaaagct ataaagagcc aacactcgct 1440
tcaaagctaa gaagagggga ccctttcacg gacttgtgtt tcttgaattc tcctattttc 1500
aagcagaaaa ggggtatgag atgtcctaaa agaagaacca agcaaacaca gtaa 1554

```

```

<210> 14
<211> 517
<212> PRT
<213> mosue

```

```

<400> 14

```

```

Met Ala Lys Glu Arg Cys Gln Lys Arg Ser Phe Gln Asp Thr Leu Glu
1          5          10         15

```

```

Asp Ile Lys Asn Arg Met Lys Glu Lys Arg Asn Lys Asn Leu Ala Gly
20          25          30

```

```

Ile Gly Lys Arg Lys Ser Phe Ile Val Ala Pro Gly Gln Val Pro Thr
35          40          45

```

```

Asn Thr Ala Thr Leu Leu Arg Tyr Tyr Gln Asp Asn Asn Arg Leu Leu
50          55          60

```

```

Val Leu Ala Leu Glu Asn Glu Lys Ser Lys Val Arg Glu Ala Gln Asp
65          70          75          80

```

```

Val Ile Leu Gln Leu Arg Lys Glu Cys Tyr Tyr Leu Thr Cys Gln Leu

```

Substitute_Sequence_Listing.TXT

85

90

95

Tyr Ala Leu Lys Glu Lys Leu Thr Ser Arg Gln Ser Glu Glu Thr Thr
100 105 110

Gln Asn Trp Lys Gly Arg Pro Ser Asp Val Val Ser Ser Ile Asp Asn
115 120 125

Thr Thr Arg Asp Leu Ser Gly Lys Ser Leu Gln Gln Ile Ala Val Glu
130 135 140

Glu Thr Asp Cys Pro Tyr Gln Thr Thr Glu Pro Ser Pro Ala Val Thr
145 150 155 160

Pro Glu Thr Gln Gly Cys Asp Phe Asp Ser Gly Lys Val Glu Ser Thr
165 170 175

Asp Glu Val Leu Pro Arg Thr Ile Ser Ile Arg Arg His Leu Arg Lys
180 185 190

Asp Phe Ser Asn Ile Ser His Ser Thr Thr Leu Glu Asp Cys Lys Ala
195 200 205

Ser Pro Arg Val Ala Gln Ser Leu Glu Val Lys Gly Ser Arg Cys Arg
210 215 220

Glu Val Thr Val Thr Leu His Arg Leu Glu Asn Val Cys Leu Trp Asn
225 230 235 240

Lys Asp Gln Ile Ser Leu Cys Ser Arg Leu Ile Asn Pro Ala Lys Ile
245 250 255

Thr Glu Thr Glu Val Ile Leu Ser Ser Lys Pro Glu Gln Ile Glu Ser
260 265 270

Lys His Lys Arg Ala Arg Lys Arg Arg Ala Glu Gln Arg Arg Thr Lys
275 280 285

Gln Arg Cys Lys Ser Lys Ser Ser Leu Arg Ser Lys Gly Asn Lys Asn
290 295 300

Lys Asp Lys Gln Gly Leu Pro Pro Thr Thr Leu Asp Gly Gly Ile Gly
305 310 315 320

Ser Cys Asp Ala Tyr Asp Phe Asn Leu Lys Gly Thr Val His Pro Thr
325 330 335

Substitute_Sequence_Listing.TXT

Pro Phe Arg Gln Lys Met Asn Asn Gly Cys Asn Lys Glu Thr Asp Ser
340 345 350

Ser Asn Ser Glu Val Ser Asp Leu Glu Cys Ser Thr Ser Glu Asp Glu
355 360 365

Ser Asp Asp Leu Tyr Leu Pro Pro Ser Lys Arg Leu Arg Asp Tyr Arg
370 375 380

Glu Ser Glu Arg Ala Val Thr Arg Pro Arg Ser Lys Arg Gly Leu Gln
385 390 400

Tyr Pro Asp Gly Lys Glu Arg Lys Glu Val Leu Pro Ser Thr Ala Pro
405 410 415

Thr Gly Ile Pro Pro Glu Thr Gln Glu Ser Pro Arg Cys Ser Leu Lys
420 425 430

Asp Val Thr Asn Ile Leu Gln Cys Pro Arg Val Lys Ile Arg Lys Pro
435 440 445

Ser Leu Pro Pro Lys Arg Arg Glu Asp Ser Pro Ala Val Ala Leu Thr
450 455 460

Lys Arg Arg Cys Ser Thr Ile Lys Ser Tyr Lys Glu Pro Thr Leu Ala
465 470 475 480

Ser Lys Leu Arg Arg Gly Asp Pro Phe Thr Asp Leu Cys Phe Leu Asn
485 490 495

Ser Pro Ile Phe Lys Gln Lys Arg Gly Met Arg Cys Pro Lys Arg Arg
500 505 510

Thr Lys Gln Thr Gln
515

<210> 15

<211> 3495

<212> DNA

<213> mouse

<400> 15

atggagtacc caggataaa agttgacact gttacctctg gaattcagag acgagtgaag 60

ggcagaattg caaagacaaa tttgaatggt tctcttgctt caaagatcaa agcaaaaata 120

ttaaacaatt cttctatctt caagatctct ctaaagcaca acaacagagc attagcgcg 180

gcccttagta aagagaaaga gaattctcga agaattacta ccgaaaagat gcaattacag 240

aaagaagtag agaaactgaa ttttgagaat acctttcttc gcttaaagtt aaataccttg 300

Substitute_Sequence_Listing.TXT

aataagaagc	ttgtagaaat	agaatcgcat	gtgagcaatg	atttggttaac	tgcaattgaa	360
ataagcagtc	tttctgagtt	ccaccaaggt	tcttttctcc	tgtcagctac	caagaaacaa	420
aggaacagta	agcagtgcaa	gcctgcgcat	cttccatatg	caagagttct	gttaacttca	480
gaaaatgatg	atgatgatgg	tgctgatgat	aatggcaga	caaagtgtaa	caacagaact	540
atatcaaaga	cctcacctga	tagtacctct	tcagtatcaa	gacaaccttc	atccttacat	600
cagtgcgaatt	tgaaagcatt	ccctcctaaa	gaagataatc	agaagacatg	tgggtcaggt	660
catttagaac	atacttcaag	tgttgatata	cttcctaata	agagccactc	agatcaaagt	720
cctaagagtt	ctctgagtga	gatgaaaact	gctccatctc	ccagcctcag	aagggaaaaa	780
ttatcacatg	gtaatgtgac	tatgaggaag	aagtgtgtgt	cttcaactcc	agacattctg	840
tatgtgacag	atttagatca	ccaaccaact	tcaagtccag	gatcaaattg	gaataatgag	900
atacatggtc	atactaata	aaccagcaat	aacacgcaa	gaaatgccga	gtgttttctt	960
gacttacctt	ctgagtcttc	cagtgagcct	gacgcaaagc	gcatggagct	agtgcagaag	1020
aacaccgata	gctttcactt	ccagaaaact	gtatatgatg	ccgctgatat	ggagttaact	1080
gctactgaca	taggcaagat	tgtagcagtt	tcaaaaagca	agaaaaatca	aaataagaaa	1140
aaggcagact	gtagaaagga	gactttcaga	aaagtgaag	gtgcaagctc	tgataaaaag	1200
agagaaaagct	caaagagaga	atgtaaagat	ggttcagaag	taggtgctga	ggaagaggct	1260
gatgcagcca	gagcagaaag	aggcgctggt	gtcctggatg	gcagagggga	ttcagaagag	1320
ccaaactgca	tttccagtac	tgagcagcca	tctcaggtaa	acacgcaaaa	gaaaagaacc	1380
ctccagaaca	gctcagatca	ggagaacatt	caaaatacga	agaggaggca	aacatatacg	1440
acagatgagc	aagaggaaac	aaaccctttc	tccagacatt	cagtcaaatt	tcttcaagat	1500
ggtaaatttg	atctgtgtca	gaaaacccta	catcataatt	taagtaagcc	ttctcgacag	1560
acattttgtga	ttcgtaaagtc	agaaaaagat	aacttatttc	caaatcaaga	agataaagac	1620
accattttctg	aaaacctaga	agttacaaat	gaatttcata	tagatgatct	ttccatcgaa	1680
gctaatagaaa	atgtatgtga	ccatgagact	cagacaatgt	tggacttgaa	aaagtctgtc	1740
agtgtctaac	aaaatcaaac	aaaaataaat	aagactaagc	agaaaataaa	tcgaaggaca	1800
aaaataattt	ctgtcatgag	ccaagtatat	gaggacaatg	ataaagatat	tcacgtccta	1860
gaaaaagaca	actttccctt	tcatacccaa	gcaaataaag	aaaccaccag	tggaaacctta	1920
gaaagttcaa	aagaatttga	atcacctctt	cttttcacaa	gagacaacgg	aagcttacgt	1980
gactgtaaga	cccagaatgt	tctggatctg	cacaagcaaa	ttcctgatct	ataccctgat	2040
cggaatgagt	cccagattag	caaaatccct	aggcaaaaag	taaatcgcaa	gacagaagta	2100
atttctggag	tgaaatgttt	tagtaatgac	caaggtgttc	attgctcaga	aaaggataag	2160

Substitute_Sequence_Listing.TXT

tctttgttac	tacaaaagga	taaagacttc	ccaggaactt	taaaagactt	aagtgagttt	2220
gatacgcttg	ctttttgtaa	caaagatagt	gcaaagtcgt	gtgattataa	gtctgaaatg	2280
ctcttggggt	tgaaaaaaca	tgaccctaata	atgcaacctg	cttgtcaaga	tgattcaaaa	2340
gcaggtaaga	aacttagaca	aaaggtaaata	cgaaaaacag	aaataatttc	taaaatcacc	2400
caaatacatg	aaaatgatag	aggaagtaca	catgactcat	taaataagaa	gctctgtcag	2460
aagggttaata	tatcaaaaat	cattttctcaa	atgaaccaa	tatatgagac	tattaatgaa	2520
gatggaaatg	gctttaaaag	ctctatcaaa	gattgcaag	atattaaaag	ttgtgacttt	2580
ggggaaatca	acagtaataa	aaaggaaaat	tatgatccaa	ttcaagatcc	ttgcacactg	2640
gttaaaaaaa	caaagagaaa	gggatcatgt	aaagcaggga	gcagtttggc	aggagctaag	2700
aacagggtgtg	gtttgcagtt	aacagactct	tcccagggtac	agtctgtccc	cttagactct	2760
ggcttaagac	accatccaaa	cgaagcagat	tctggtcctg	gagagcagac	taacctgcca	2820
aagatgcaga	aacaaagcgc	tgggaggtca	ctgggagatg	ctttctctgt	gagtctggga	2880
aaagaaggaa	gccgcccagc	caaagcagtt	agtaaaatga	cacccaaatc	aaagaagaga	2940
aagctccctc	tcggttgttc	tcctgaaacc	cacgggacgg	tggagataac	acccaacact	3000
gacctcgcta	aggctgttga	ctcccaacag	actgagaagg	agaactatct	ggagaaggag	3060
aaaattgcca	agaggaagcc	agatttttgt	acaaaggtgt	tgaaaccttt	atctgagaca	3120
tgttcatcta	acataaagaa	ttcttccttg	gacagtatgt	gtaagagttc	gctacctttg	3180
agtatttctt	ctagaaaaac	cctgatgctg	gaagaaagtt	cttccttgga	gagtacatgc	3240
atctttcaag	taggtgatgc	cgctcatgag	aagataacga	caggcacacg	taatccccac	3300
cacaggacac	agaagtcgac	accgggtagc	agaacgtccc	tggctttggt	ggataaccagt	3360
tctgtttcag	ataccaaccc	tgctaacccc	gagaatgagt	cagaagggca	gtcttcacac	3420
ccaatgagaa	ggaaaagaca	gtgcgtccct	ctcaacctga	cagagccaag	ccttagaagc	3480
aagatgagga	gataa					3495

<210> 16
 <211> 1164
 <212> PRT
 <213> mouse

<400> 16

Met Glu Tyr Pro Gly Ile Lys Val Asp Thr Val Thr Ser Gly Ile Gln
 1 5 10 15

Arg Arg Val Lys Gly Arg Ile Ala Lys Thr Asn Leu Asn Val Ser Leu
 20 25 30

Ala Ser Lys Ile Lys Ala Lys Ile Leu Asn Asn Ser Ser Ile Phe Lys

Substitute_Sequence_Listing.TXT

35

40

45

Ile Ser Leu Lys His Asn Asn Arg Ala Leu Ala Arg Ala Leu Ser Lys
50 55 60

Glu Lys Glu Asn Ser Arg Arg Ile Thr Thr Glu Lys Met Gln Leu Gln
65 70 75 80

Lys Glu Val Glu Lys Leu Asn Phe Glu Asn Thr Phe Leu Arg Leu Lys
85 90 95

Leu Asn Thr Leu Asn Lys Lys Leu Val Glu Ile Glu Ser His Val Ser
100 105 110

Asn Asp Leu Leu Thr Ala Ile Glu Ile Ser Ser Leu Ser Glu Phe His
115 120 125

Gln Gly Ser Phe Leu Leu Ser Ala Thr Lys Lys Gln Arg Asn Ser Lys
130 135 140

Gln Cys Lys Pro Ala His Leu Pro Tyr Ala Arg Val Leu Leu Thr Ser
145 150 155 160

Glu Asn Asp Asp Asp Asp Gly Ala Asp Asp Lys Trp Gln Thr Lys Cys
165 170 175

Asn Asn Arg Thr Ile Ser Lys Thr Ser Pro Asp Ser Thr Ser Ser Val
180 185 190

Ser Arg Gln Pro Ser Ser Leu His Gln Cys Asn Leu Lys Ala Phe Pro
195 200 205

Pro Lys Glu Asp Asn Gln Lys Thr Cys Gly Ser Gly His Leu Glu His
210 215 220

Thr Ser Ser Val Asp Ile Leu Pro Asn Glu Ser His Ser Asp Gln Ser
225 230 235 240

Pro Lys Ser Ser Leu Ser Glu Met Lys Thr Ala Pro Ser Pro Ser Leu
245 250 255

Arg Arg Glu Lys Leu Ser His Gly Asn Val Thr Met Arg Lys Lys Cys
260 265 270

Val Ser Ser Thr Pro Asp Ile Leu Tyr Val Thr Asp Leu Asp His Gln
275 280 285

Substitute_Sequence_Listing.TXT

Pro Thr Ser Ser Pro Gly Ser Asn Trp Asn Asn Glu Ile His Gly His
290 295 300

Thr Asn Glu Thr Ser Asn Asn Thr Gln Arg Asn Ala Glu Cys Phe Leu
305 310 315 320

Asp Leu Pro Ser Glu Ser Ser Ser Glu Pro Asp Ala Lys Arg Met Glu
325 330 335

Leu Val Gln Lys Asn Thr Asp Ser Phe His Phe Gln Lys Thr Val Tyr
340 345 350

Asp Ala Ala Asp Met Glu Leu Thr Ala Thr Asp Ile Gly Lys Ile Val
355 360 365

Ala Val Ser Lys Ser Lys Lys Asn Gln Asn Lys Lys Lys Ala Asp Cys
370 375 380

Arg Lys Glu Thr Phe Arg Lys Val Lys Gly Ala Ser Ser Asp Lys Lys
385 390 395 400

Arg Glu Ser Ser Lys Arg Glu Cys Lys Asp Gly Ser Glu Val Gly Ala
405 410 415

Glu Glu Glu Ala Asp Ala Ala Arg Ala Glu Arg Gly Ala Gly Val Leu
420 425 430

Asp Gly Arg Gly Asp Ser Glu Glu Pro Asn Cys Ile Ser Ser Thr Glu
435 440 445

Gln Pro Ser Gln Val Asn Thr Gln Lys Lys Arg Thr Leu Gln Asn Ser
450 455 460

Ser Asp Gln Glu Asn Ile Gln Asn Thr Lys Arg Arg Gln Thr Tyr Thr
465 470 475 480

Thr Asp Glu Gln Glu Glu Thr Asn Pro Phe Ser Arg His Ser Val Lys
485 490 495

Phe Leu Gln Asp Gly Lys Phe Asp Leu Cys Gln Lys Thr Leu His His
500 505 510

Asn Leu Ser Lys Pro Ser Arg Gln Thr Phe Val Ile Arg Lys Ser Glu
515 520 525

Lys Asp Asn Leu Phe Pro Asn Gln Glu Asp Lys Asp Thr Ile Ser Glu
530 535 540

Substitute_Sequence_Listing.TXT

```

Asn Leu Glu Val Thr Asn Glu Phe His Ile Asp Asp Leu Ser Ile Glu
545          550          555          560

Ala Asn Glu Asn Val Cys Asp His Glu Thr Gln Thr Met Leu Asp Leu
          565          570          575

Lys Lys Ser Val Ser Ala Gln Gln Asn Gln Thr Lys Ile Asn Lys Thr
          580          585          590

Lys Gln Lys Ile Asn Arg Arg Thr Lys Ile Ile Ser Val Met Ser Gln
          595          600          605

Val Tyr Glu Asp Asn Asp Lys Asp Ile His Val Leu Glu Lys Asp Asn
610          615          620

Phe Pro Phe His Thr Gln Ala Asn Lys Glu Thr Thr Ser Gly Asn Leu
625          630          635          640

Glu Ser Ser Lys Glu Phe Glu Ser Pro Leu Leu Phe Thr Arg Asp Asn
          645          650          655

Gly Ser Leu Arg Asp Cys Lys Thr Gln Asn Val Leu Asp Leu His Lys
          660          665          670

Gln Ile Pro Asp Leu Tyr Pro Asp Arg Asn Glu Ser Gln Ile Ser Lys
          675          680          685

Ile Pro Arg Gln Lys Val Asn Arg Lys Thr Glu Val Ile Ser Gly Val
690          695          700

Lys Cys Phe Ser Asn Asp Gln Gly Val His Cys Ser Glu Lys Asp Lys
705          710          715          720

Ser Leu Leu Leu Gln Lys Asp Lys Asp Phe Pro Gly Thr Leu Lys Asp
          725          730          735

Leu Ser Glu Phe Asp Thr Pro Ala Phe Cys Asn Lys Asp Ser Ala Lys
          740          745          750

Ser Cys Asp Tyr Lys Ser Glu Met Leu Leu Gly Leu Lys Lys His Asp
755          760          765

Pro Asn Met Gln Pro Ala Cys Gln Asp Asp Ser Lys Ala Gly Lys Lys
770          775          780

Leu Arg Gln Lys Val Asn Arg Lys Thr Glu Ile Ile Ser Lys Ile Thr
785          790          795          800

```

Substitute_Sequence_Listing.TXT

Gln Ile His Glu Asn Asp Arg Gly Ser Thr His Asp Ser Leu Asn Lys
805 810 815

Lys Leu Cys Gln Lys Val Asn Ile Ser Lys Ile Ile Ser Gln Met Asn
820 825 830

Gln Ile Tyr Glu Thr Ile Asn Glu Asp Gly Asn Gly Phe Lys Ser Ser
835 840 845

Ile Lys Asp Cys Glu Asp Ile Lys Ser Cys Asp Phe Gly Glu Ile Asn
850 855 860

Ser Asn Lys Lys Glu Asn Tyr Asp Pro Ile Gln Asp Pro Cys Thr Leu
865 870 875 880

Val Lys Lys Thr Lys Arg Lys Gly Ser Cys Lys Ala Gly Ser Ser Leu
885 890 895

Ala Gly Ala Lys Asn Arg Cys Gly Leu Gln Leu Thr Asp Ser Ser Gln
900 905 910

Val Gln Ser Val Pro Leu Asp Ser Gly Leu Arg His His Pro Asn Glu
915 920 925

Ala Asp Ser Gly Pro Gly Glu Gln Thr Asn Leu Pro Lys Met Gln Lys
930 935 940

Gln Ser Ala Gly Arg Ser Leu Gly Asp Ala Phe Ser Val Ser Leu Gly
945 950 955 960

Lys Glu Gly Ser Arg Pro Ala Lys Ala Val Ser Lys Met Thr Pro Lys
965 970 975

Ser Lys Lys Arg Lys Leu Pro Leu Gly Cys Ser Pro Glu Thr His Gly
980 985 990

Thr Val Glu Ile Thr Pro Asn Thr Asp Leu Ala Lys Ala Val Asp Ser
995 1000 1005

Gln Gln Thr Glu Lys Glu Asn Tyr Leu Glu Lys Glu Lys Ile Ala
1010 1015 1020

Lys Arg Lys Pro Asp Phe Cys Thr Lys Val Leu Lys Pro Leu Ser
1025 1030 1035

Glu Thr Cys Ser Ser Asn Ile Lys Asn Ser Ser Leu Asp Ser Met

Substitute_Sequence_Listing.TXT

1040

1045

1050

Cys Lys Ser Ser Leu Pro Leu Ser Ile Ser Ser Arg Lys Thr Leu
1055 1060 1065
Met Leu Glu Glu Ser Ser Ser Leu Glu Ser Thr Cys Ile Phe Gln
1070 1075 1080
Val Gly Asp Ala Ala His Glu Lys Ile Thr Thr Gly Thr Arg Asn
1085 1090 1095
Pro His His Arg Thr Gln Lys Ser Thr Pro Gly Ser Arg Thr Ser
1100 1105 1110
Leu Val Leu Val Asp Thr Ser Ser Val Ser Asp Thr Asn Pro Ala
1115 1120 1125
Asn Pro Glu Asn Glu Ser Glu Gly Gln Ser Ser His Pro Met Arg
1130 1135 1140
Arg Lys Arg Gln Cys Val Pro Leu Asn Leu Thr Glu Pro Ser Leu
1145 1150 1155
Arg Ser Lys Met Arg Arg
1160

<210> 17
<211> 1584
<212> DNA
<213> Homo sapiens

<400> 17
atggccaagg aaagatgcct gaaaaagtcc tttcaagata gtcttgaaga cataaagaag 60
cgaatgaaag agaaaaggaa taaaaacttg gcagagattg gcaaacgcag gtcttttata 120
gctgcaccat gccaaataat caccaacact tctacactgc tgaaaaatta ccaagacaac 180
aacaaaatgt tagtttttagc tttggaaaat gaaaaatcca aagtgaaaga agcccaagat 240
atcatcctac agctgagaaa agaatgttac tatctcacat gtcagctata tgcattgaaa 300
ggaaaactta catcacaaca aacagtagaa cctgctcaga accaggaaat atgttcctct 360
ggaatggacc ccaatagtga tgacagctcc agaaatttat ttgtgaagga tttaccgcaa 420
attcctcttg aagaaactga acttccagga caaggagaat catttcaaat agaagatcag 480
atacctacta ttcctcaaga cacactggga gttgattttg attcaggtga agctaagtct 540
actgataatg tcttacctag aactgtatct gttcgtagca gtttaaagaa acattgtaac 600
agtatatgtc agtttgatag cttggatgat tttgaaacca gtcatttggc agggaagtct 660

Substitute_Sequence_Listing.TXT

```

tttgaattcg aaagagttgg attttttagac ccactagtaa acatgcacat acctgaaaat 720
gtacaacaca atgcttgtca atggagcaag gaccaagtta acttatcacc aaagctgatt 780
cagccaggaa cgtttactaa aacaaaagaa gacatttttag aatctaaatc tgaacaaact 840
aaaagtaagc aaagagatac acaagaaaga aaaagagaag agaaaagaaa agctaacagg 900
agaaaatcaa aacgtatgtc aaaatataaa gagaataaaa gcgaaaataa aaaaactggt 960
ccccaaaaaa aaatgcacaa atctgtcagt tccaatgatg cttacaattt taatttgtaa 1020
gaggggtgtc atcttactcc tttccgacaa aaagtgagca atgactctaa tagagaagaa 1080
aacaacgagt ctgaagtgag cctctgtgaa tcaagtgggt caggagatga ttccgatgac 1140
ctctattttg ccacttgcaa gtacattcag aatcccacga gcaattcaga tagaccagtc 1200
accaggcctc tagctaaaag agcactgaaa tacacagatg aaaaagagac ggaggggttct 1260
aagccaacaa aaactcctac cactacacca cctgaaactc agcagtcacc tcactcttagc 1320
ctgaaggata tcaccaatgt ctcttctgtat cctgttgtga aaatcagaag actttctctt 1380
tctccaaaaa agaataaagc aagcccagca gtggctctgc ctaaacgtag gtgcacagcc 1440
agcgtgaact ataaggagcc caccctcgct tcgaaactga gaagagggga cccttttaca 1500
gatttgtgtt ttttgaattc tcctattttc aagcagaaaa aggatttgag acgttctaaa 1560
aaaagtatga aacaaataca atga 1584

```

```

<210> 18
<211> 527
<212> PRT
<213> Homo sapiens

```

<400> 18

```

Met Ala Lys Glu Arg Cys Leu Lys Lys Ser Phe Gln Asp Ser Leu Glu
1          5          10          15

```

```

Asp Ile Lys Lys Arg Met Lys Glu Lys Arg Asn Lys Asn Leu Ala Glu
20          25          30

```

```

Ile Gly Lys Arg Arg Ser Phe Ile Ala Ala Pro Cys Gln Ile Ile Thr
35          40          45

```

```

Asn Thr Ser Thr Leu Leu Lys Asn Tyr Gln Asp Asn Asn Lys Met Leu
50          55          60

```

```

Val Leu Ala Leu Glu Asn Glu Lys Ser Lys Val Lys Glu Ala Gln Asp
65          70          75          80

```

```

Ile Ile Leu Gln Leu Arg Lys Glu Cys Tyr Tyr Leu Thr Cys Gln Leu
85          90          95

```


Substitute_Sequence_Listing.TXT

Tyr Ala Leu Lys Gly Lys Leu Thr Ser Gln Gln Thr Val Glu Pro Ala
 100 105 110
 Gln Asn Gln Glu Ile Cys Ser Ser Gly Met Asp Pro Asn Ser Asp Asp
 115 120 125
 Ser Ser Arg Asn Leu Phe Val Lys Asp Leu Pro Gln Ile Pro Leu Glu
 130 135 140
 Glu Thr Glu Leu Pro Gly Gln Gly Glu Ser Phe Gln Ile Glu Asp Gln
 145 150 155 160
 Ile Pro Thr Ile Pro Gln Asp Thr Leu Gly Val Asp Phe Asp Ser Gly
 165 170 175
 Glu Ala Lys Ser Thr Asp Asn Val Leu Pro Arg Thr Val Ser Val Arg
 180 185 190
 Ser Ser Leu Lys Lys His Cys Asn Ser Ile Cys Gln Phe Asp Ser Leu
 195 200 205
 Asp Asp Phe Glu Thr Ser His Leu Ala Gly Lys Ser Phe Glu Phe Glu
 210 215 220
 Arg Val Gly Phe Leu Asp Pro Leu Val Asn Met His Ile Pro Glu Asn
 225 230 235 240
 Val Gln His Asn Ala Cys Gln Trp Ser Lys Asp Gln Val Asn Leu Ser
 245 250 255
 Pro Lys Leu Ile Gln Pro Gly Thr Phe Thr Lys Thr Lys Glu Asp Ile
 260 265 270
 Leu Glu Ser Lys Ser Glu Gln Thr Lys Ser Lys Gln Arg Asp Thr Gln
 275 280 285
 Glu Arg Lys Arg Glu Glu Lys Arg Lys Ala Asn Arg Arg Lys Ser Lys
 290 295 300
 Arg Met Ser Lys Tyr Lys Glu Asn Lys Ser Glu Asn Lys Lys Thr Val
 305 310 315 320
 Pro Gln Lys Lys Met His Lys Ser Val Ser Ser Asn Asp Ala Tyr Asn
 325 330 335
 Phe Asn Leu Glu Glu Gly Val His Leu Thr Pro Phe Arg Gln Lys Val
 340 345 350

Substitute_Sequence_Listing.TXT

Ser Asn Asp Ser Asn Arg Glu Glu Asn Asn Glu Ser Glu Val Ser Leu
355 360 365

Cys Glu Ser Ser Gly Ser Gly Asp Asp Ser Asp Asp Leu Tyr Leu Pro
370 375 380

Thr Cys Lys Tyr Ile Gln Asn Pro Thr Ser Asn Ser Asp Arg Pro Val
385 390 395 400

Thr Arg Pro Leu Ala Lys Arg Ala Leu Lys Tyr Thr Asp Glu Lys Glu
405 410 415

Thr Glu Gly Ser Lys Pro Thr Lys Thr Pro Thr Thr Thr Pro Pro Glu
420 425 430

Thr Gln Gln Ser Pro His Leu Ser Leu Lys Asp Ile Thr Asn Val Ser
435 440 445

Leu Tyr Pro Val Val Lys Ile Arg Arg Leu Ser Leu Ser Pro Lys Lys
450 455 460

Asn Lys Ala Ser Pro Ala Val Ala Leu Pro Lys Arg Arg Cys Thr Ala
465 470 475 480

Ser Val Asn Tyr Lys Glu Pro Thr Leu Ala Ser Lys Leu Arg Arg Gly
485 490 495

Asp Pro Phe Thr Asp Leu Cys Phe Leu Asn Ser Pro Ile Phe Lys Gln
500 505 510

Lys Lys Asp Leu Arg Arg Ser Lys Lys Ser Met Lys Gln Ile Gln
515 520 525

<210> 19

<211> 3798

<212> DNA

<213> Homo sapiens

<400> 19

atggagtgcc cagtgatgga aactggctca ctttttacct caggaattaa gagacatttg 60

aaagacaaaa gaatttcaaa gactactaag ttgaatgttt ctcttgcttc aaaaataaaa 120

acaaaaatac taaataattc ttctattttc aaaatatctt taaagcacia caacagggca 180

ttagctcagg ctcttagtag agaaaaagag aattctcgaa gaattacaac tgaaaagatg 240

ctattgcaaa aagaagtaga gaaactgaat ttgagaaca catttcttcg cctaaagcta 300

aataacttga ataagaagct tatagacata gaagctctca tgaacaataa cttgataact 360

Substitute_Sequence_Listing.TXT

gcaactgaaa	tgagcagtct	ttctgagttc	catcagagtt	cctttctact	gtcagctagc	420
aagaagaaac	gagttagtaa	acagtgcaag	ttgatgcgtc	ttccatttgc	aagggttcca	480
ttaacttcaa	atgatgatga	agatgaagat	aaagagaaaa	tgcagtgtga	caacaatatt	540
aaatcaaaga	cattacctga	tattccctct	tcaggatcaa	caacacaacc	tttatcaact	600
caggataatt	cggaagtgtt	atttcttaaa	gaaaataatc	aaaatgtata	tggtttagat	660
gattcagaac	atatttcttc	tatagttgat	gtacctcca	gagaaagcca	ttcccactca	720
gaccaaagt	ctaagacttc	tctaattgag	gagatgagaa	acgcccagtc	tattggccgc	780
agatgggaga	aaccatctcc	tagtaatgtg	actgaaagga	agaagcgtgg	gtcatcttgg	840
gaatcaaata	atctttctgc	agacactccc	tgtgcaacag	ttttagataa	acaacacatt	900
tcaagtccag	aattaaattg	caataatgag	ataaatggtc	atactaata	aacaaatact	960
gaaatgcaaa	gaaataaaca	ggatcttcct	ggcttatctt	ctgagtctgc	cagagaacct	1020
aatgcagagt	gcatgaatca	aattgaggat	aatgatgact	ttcaattgca	gaaaactgtg	1080
tatgatgctg	acatggattt	aactgctagt	gaagtcagca	aaattgtcac	agtctcaaca	1140
ggcattaaaa	agaaaagtaa	taaaaaaaca	aatgaacatg	gaatgaaaac	tttcagaaaa	1200
gtgaaagatt	ccagctctga	aaaaaagaga	gaaagatcaa	agagacagtt	taaaaatagt	1260
tcagatgtcg	atattgggga	aaagattgaa	aacaggacag	aaagatctga	tgtcctggat	1320
ggcaaaagg	gtgcagaaga	tcccggtttt	attttcaata	atgaacagct	ggctcagatg	1380
aatgaacagc	tggctcaggt	gaatgaacta	aagaaaatga	cccttcaaac	tggctttgaa	1440
caaggtgaca	gagaaaatgt	actgtgtaat	aaaaaggaga	aaagaataac	aatgagcaa	1500
gaggaaacat	actctttatc	ccaaagttca	ggtaaatttc	accaggagag	taaatttgat	1560
aagggtcaga	attccctaac	ttgtaataaa	agtaaagctt	ctagacagac	atttgtgatt	1620
cacaaattag	aaaaagataa	cttactccca	aaccaaagg	ataaagtaac	catttatgaa	1680
aacctagacg	tcacaaatga	atttcacaca	gccaatcttt	ccaccaaaga	taatggaaat	1740
ttatgtgatt	atgggaccca	caatatattg	gatttgaaaa	agtatgtcac	tgatattcaa	1800
ccctcagagc	aaaatgaatc	aaacattaat	aagcttagaa	agaaagtaaa	ccggaagaca	1860
gaaataat	ctggaatgaa	ccacatgtat	gaagataatg	ataaagatgt	ggtgcatggc	1920
ctaaaaaaag	gtaatttttt	tttcaaaacc	caagaggata	aagaacctat	ctctgaaaac	1980
atagaagttt	caaagagct	tcaaattcca	gctctttcta	ctagagataa	tgaaaatcaa	2040
tgtgactata	ggaccagaa	tgtgttgggt	ttgcaaaagc	agatcaccaa	tatgtacccc	2100
gttcagcaaa	atgaatcaaa	agttaataag	aagcttaggc	agaaagtaaa	tcggaagaca	2160
gaaataat	ctgaagtga	tcatttagat	aatgacaaaa	gtatagaata	cacagttaaa	2220

Substitute_Sequence_Listing.TXT

agtcactcac tctttttaac gcaaaaagat aaggaaataa tccccggaaa cctagaagac	2280
ccaagtgagt ttgaaacacc tgctctttct accaaagata gtggaaacct gtatgattct	2340
gagattcaaa atgttttggg ggtgaaacat ggccatgata tgcaacctgc ttgtcaaaat	2400
gattcaaaaa taggtaagaa gcctagacta aatgtatgtc aaaagtcaga aataattcct	2460
gaaaccaacc aaatatatga gaatgataac aaagggtgtac atgacctaga aaaagataac	2520
ttcttctctc taaccccaaa ggataaagaa acaatttctg aaaatctaca agtcacaaat	2580
gaatttcaaa cagttgatct tctcatcaaa gataatggaa atttatgtga ttatgacacc	2640
cagaatatat tggagttgaa aaagtatggt actgatagga aatctgctga gcaaaatgaa	2700
tcaaaaataa ataagctcag gaataaagtg aattggaaga cagaaataat ttctgaaatg	2760
aaccagatat atgaggataa tgataaagat gcacatgtcc aagaaagcta tacaaaagat	2820
cttgatttta aagtaaataa atctaacaac aaacttgaat gccaagacat tatcaataaa	2880
cactatatgg aagtcaacag taatgaaaag gaaagttgtg atcaaatttt agattcctac	2940
aaagtagtta aaaaacgtaa gaaagaatca tcatgcaagg caaagaacat tttgacaaaa	3000
gctaagaaca aacttgcttc acagttaaca gaatcttcac agacatctat ctccttagaa	3060
tctgatttaa aacatattac tagtgaagca gattctgatc caggaaaccc agttgaacta	3120
tgtaagactc agaagcaaag cactaccact ttgaataaaa aagatctccc ttttgtggaa	3180
gaaataaaaag aaggagagtg tcaggttaaa aaggtaaata aaatgacatc taagtcaaag	3240
aaaaggaaga cctccataga tccttctcca gagagccatg aagtaatgga aagaatactt	3300
gacagcgttc agggaagtc tactgtatct gaacaagctg ataaggaaaa caatttgag	3360
aatgagaaaa tgggtcaaaa taagccagac ttttacacaa aggcatttag atctttgtct	3420
gagatacatt cacctaacat acaagattct tcctttgaca gtgttcgtga aggttttagta	3480
cctttgagcg tttcttctgg taaaaatgtg ataataaaaag aaaattttgc cttggagtgc	3540
tccccagcct ttcaagtaag tgatgatgag catgagaaga tgaacaagat gaaatttaaa	3600
gtcaaccgga gaacccaaaa atcaggaata ggtgatagac cattacagga cttgtcaa	3660
accagttttg tttcaataa cactgctgaa tctgaaaata agtcagaaga tctatcttca	3720
gaacggacaa gcagaagaag aagggtgtact cctttctatt ttaaagagcc aagcctcaga	3780
gacaagatga gaagatga	3798

<210> 20
 <211> 1265
 <212> PRT
 <213> Homo sapiens

<400> 20

Met Glu Cys Pro Val Met Glu Thr Gly Ser Leu Phe Thr Ser Gly Ile

Substitute_Sequence_Listing.TXT

```

1           5           10           15
Lys Arg His Leu Lys Asp Lys Arg Ile Ser Lys Thr Thr Lys Leu Asn
20           25           30
Val Ser Leu Ala Ser Lys Ile Lys Thr Lys Ile Leu Asn Asn Ser Ser
35           40           45
Ile Phe Lys Ile Ser Leu Lys His Asn Asn Arg Ala Leu Ala Gln Ala
50           55           60
Leu Ser Arg Glu Lys Glu Asn Ser Arg Arg Ile Thr Thr Glu Lys Met
65           70           75           80
Leu Leu Gln Lys Glu Val Glu Lys Leu Asn Phe Glu Asn Thr Phe Leu
85           90           95
Arg Leu Lys Leu Asn Asn Leu Asn Lys Lys Leu Ile Asp Ile Glu Ala
100          105          110
Leu Met Asn Asn Asn Leu Ile Thr Ala Ile Glu Met Ser Ser Leu Ser
115          120          125
Glu Phe His Gln Ser Ser Phe Leu Leu Ser Ala Ser Lys Lys Lys Arg
130          135          140
Ile Ser Lys Gln Cys Lys Leu Met Arg Leu Pro Phe Ala Arg Val Pro
145          150          155          160
Leu Thr Ser Asn Asp Asp Glu Asp Glu Asp Lys Glu Lys Met Gln Cys
165          170          175
Asp Asn Asn Ile Lys Ser Lys Thr Leu Pro Asp Ile Pro Ser Ser Gly
180          185          190
Arg Thr Thr Gln Pro Leu Ser Thr Gln Asp Asn Ser Gly Val Leu Phe
195          200          205
Leu Lys Glu Asn Asn Gln His Val Tyr Gly Leu Asp Asp Ser Glu His
210          215          220
Ile Ser Ser Ile Val Asp Val Pro Pro Arg Glu Ser His Ser His Ser
225          230          235          240
Asp Gln Ser Ser Lys Thr Ser Leu Met Ser Glu Met Arg Asn Ala Gln
245          250          255

```

Substitute_Sequence_Listing.TXT

Ser Ile Gly Arg Arg Trp Glu Lys Pro Ser Pro Ser Asn Val Thr Glu
260 265 270

Arg Lys Lys Arg Gly Ser Ser Trp Glu Ser Asn Asn Leu Ser Ala Asp
275 280 285

Thr Pro Cys Ala Thr Val Leu Asp Lys Gln His Ile Ser Ser Pro Glu
290 295 300

Leu Asn Cys Asn Asn Glu Ile Asn Gly His Thr Asn Glu Thr Asn Thr
305 310 315 320

Glu Met Gln Arg Asn Lys Gln Asp Leu Pro Gly Leu Ser Ser Glu Ser
325 330 335

Ala Arg Glu Pro Asn Ala Glu Cys Met Asn Gln Ile Glu Asp Asn Asp
340 345 350

Asp Phe Gln Leu Gln Lys Thr Val Tyr Asp Ala Asp Met Asp Leu Thr
355 360 365

Ala Ser Glu Val Ser Lys Ile Val Thr Val Ser Thr Gly Ile Lys Lys
370 375 380

Lys Ser Asn Lys Lys Thr Asn Glu His Gly Met Lys Thr Phe Arg Lys
385 390 395 400

Val Lys Asp Ser Ser Ser Glu Lys Lys Arg Glu Arg Ser Lys Arg Gln
405 410 415

Phe Lys Asn Ser Ser Asp Val Asp Ile Gly Glu Lys Ile Glu Asn Arg
420 425 430

Thr Glu Arg Ser Asp Val Leu Asp Gly Lys Arg Gly Ala Glu Asp Pro
435 440 445

Gly Leu Phe Phe Asn Asn Glu Gln Leu Ala Gln Met Asn Glu Gln Leu
450 455 460

Ala Gln Val Asn Glu Leu Lys Lys Met Thr Leu Gln Thr Gly Phe Glu
465 470 475 480

Gln Gly Asp Arg Glu Asn Val Leu Cys Asn Lys Lys Glu Lys Arg Val
485 490 495

Thr Asn Glu Gln Glu Glu Thr Tyr Ser Leu Ser Gln Ser Ser Gly Lys
500 505 510

Substitute_Sequence_Listing.TXT

Phe His Gln Glu Ser Lys Phe Asp Lys Gly Gln Asn Ser Leu Thr Cys
 515 520 525
 Asn Lys Ser Lys Ala Ser Arg Gln Thr Phe Val Ile His Lys Leu Glu
 530 535 540
 Lys Asp Asn Leu Leu Pro Asn Gln Lys Asp Lys Val Thr Ile Tyr Glu
 545 550 555 560
 Asn Leu Asp Val Thr Asn Glu Phe His Thr Ala Asn Leu Ser Thr Lys
 565 570 575
 Asp Asn Gly Asn Leu Cys Asp Tyr Gly Thr His Asn Ile Leu Asp Leu
 580 585 590
 Lys Lys Tyr Val Thr Asp Ile Gln Pro Ser Glu Gln Asn Glu Ser Asn
 595 600 605
 Ile Asn Lys Leu Arg Lys Lys Val Asn Arg Lys Thr Glu Ile Ile Ser
 610 615 620
 Gly Met Asn His Met Tyr Glu Asp Asn Asp Lys Asp Val Val His Gly
 625 630 635 640
 Leu Lys Lys Gly Asn Phe Phe Phe Lys Thr Gln Glu Asp Lys Glu Pro
 645 650 655
 Ile Ser Glu Ser Ile Glu Val Ser Lys Glu Leu Gln Ile Pro Ala Leu
 660 665 670
 Ser Thr Arg Asp Asn Glu Asn Gln Cys Asp Tyr Arg Thr Gln Asn Val
 675 680 685
 Leu Gly Leu Gln Lys Gln Ile Thr Asn Met Tyr Pro Val Gln Gln Asn
 690 695 700
 Glu Ser Lys Val Asn Lys Lys Leu Arg Gln Lys Val Asn Arg Lys Thr
 705 710 715 720
 Glu Ile Ile Ser Glu Val Asn His Leu Asp Asn Asp Lys Ser Ile Glu
 725 730 735
 Tyr Thr Val Lys Ser His Ser Leu Phe Leu Thr Gln Lys Asp Lys Glu
 740 745 750
 Ile Ile Pro Gly Asn Leu Glu Asp Pro Ser Glu Phe Glu Thr Pro Ala
 755 760 765

Substitute_Sequence_Listing.TXT

Leu Ser Thr Lys Asp Ser Gly Asn Leu Tyr Asp Ser Glu Ile Gln Asn
 770 775 780
 Val Leu Gly Val Lys His Gly His Asp Met Gln Pro Ala Cys Gln Asn
 785 790 795 800
 Asp Ser Lys Ile Gly Lys Lys Pro Arg Leu Asn Val Cys Gln Lys Ser
 805 810 815
 Glu Ile Ile Pro Glu Thr Asn Gln Ile Tyr Glu Asn Asp Asn Lys Gly
 820 825 830
 Val His Asp Leu Glu Lys Asp Asn Phe Phe Ser Leu Thr Pro Lys Asp
 835 840 845
 Lys Glu Thr Ile Ser Glu Asn Leu Gln Val Thr Asn Glu Phe Gln Thr
 850 855 860
 Val Asp Leu Leu Ile Lys Asp Asn Gly Asn Leu Cys Asp Tyr Asp Thr
 865 870 875 880
 Gln Asn Ile Leu Glu Leu Lys Lys Tyr Val Thr Asp Arg Lys Ser Ala
 885 890 895
 Glu Gln Asn Glu Ser Lys Ile Asn Lys Leu Arg Asn Lys Val Asn Trp
 900 905 910
 Lys Thr Glu Ile Ile Ser Glu Met Asn Gln Ile Tyr Glu Asp Asn Asp
 915 920 925
 Lys Asp Ala His Val Gln Glu Ser Tyr Thr Lys Asp Leu Asp Phe Lys
 930 935 940
 Val Asn Lys Ser Lys Gln Lys Leu Glu Cys Gln Asp Ile Ile Asn Lys
 945 950 955 960
 His Tyr Met Glu Val Asn Ser Asn Glu Lys Glu Ser Cys Asp Gln Ile
 965 970 975
 Leu Asp Ser Tyr Lys Val Val Lys Lys Arg Lys Lys Glu Ser Ser Cys
 980 985 990
 Lys Ala Lys Asn Ile Leu Thr Lys Ala Lys Asn Lys Leu Ala Ser Gln
 995 1000 1005
 Leu Thr Glu Ser Ser Gln Thr Ser Ile Ser Leu Glu Ser Asp Leu

Substitute_Sequence_Listing.TXT

1010													
Lys	His	Ile	Thr	Ser	Glu	Ala	Asp	Ser	Asp	Pro	Gly	Asn	Pro Val
1025						1030					1035		
Glu	Leu	Cys	Lys	Thr	Gln	Lys	Gln	Ser	Thr	Thr	Thr	Leu	Asn Lys
1040						1045					1050		
Lys	Asp	Leu	Pro	Phe	Val	Glu	Glu	Ile	Lys	Glu	Gly	Glu	Cys Gln
1055						1060					1065		
Val	Lys	Lys	Val	Asn	Lys	Met	Thr	Ser	Lys	Ser	Lys	Lys	Arg Lys
1070						1075					1080		
Thr	Ser	Ile	Asp	Pro	Ser	Pro	Glu	Ser	His	Glu	Val	Met	Glu Arg
1085						1090					1095		
Ile	Leu	Asp	Ser	Val	Gln	Gly	Lys	Ser	Thr	Val	Ser	Glu	Gln Ala
1100						1105					1110		
Asp	Lys	Glu	Asn	Asn	Leu	Glu	Asn	Glu	Lys	Met	Val	Lys	Asn Lys
1115						1120					1125		
Pro	Asp	Phe	Tyr	Thr	Lys	Ala	Phe	Arg	Ser	Leu	Ser	Glu	Ile His
1130						1135					1140		
Ser	Pro	Asn	Ile	Gln	Asp	Ser	Ser	Phe	Asp	Ser	Val	Arg	Glu Gly
1145						1150					1155		
Leu	Val	Pro	Leu	Ser	Val	Ser	Ser	Gly	Lys	Asn	Val	Ile	Ile Lys
1160						1165					1170		
Glu	Asn	Phe	Ala	Leu	Glu	Cys	Ser	Pro	Ala	Phe	Gln	Val	Ser Asp
1175						1180					1185		
Asp	Glu	His	Glu	Lys	Met	Asn	Lys	Met	Lys	Phe	Lys	Val	Asn Arg
1190						1195					1200		
Arg	Thr	Gln	Lys	Ser	Gly	Ile	Gly	Asp	Arg	Pro	Leu	Gln	Asp Leu
1205						1210					1215		
Ser	Asn	Thr	Ser	Phe	Val	Ser	Asn	Asn	Thr	Ala	Glu	Ser	Glu Asn
1220						1225					1230		
Lys	Ser	Glu	Asp	Leu	Ser	Ser	Glu	Arg	Thr	Ser	Arg	Arg	Arg Arg
1235						1240					1245		

Substitute_Sequence_Listing.TXT

Cys Thr Pro Phe Tyr Phe Lys Glu Pro Ser Leu Arg Asp Lys Met
1250 1255 1260

Arg Arg
1265

<210> 21
<211> 45
<212> PRT
<213> yeast

<400> 21

Met Glu Ser Leu Lys Lys Lys Phe Leu Lys Gln Asn Arg Glu Ile Ile
1 5 10 15

Lys Ile Asn Thr Gln Leu Ser Ile Lys Ile Arg Glu Ser Glu Asn Glu
20 25 30

Ile Gln Asp Leu Ile Gln Glu Asn Phe Thr Leu Lys Ser
35 40 45

<210> 22
<211> 45
<212> PRT
<213> yeast

<400> 22

Val Glu Asp Leu Lys Lys Lys Gln Ile Arg Gln Tyr Lys Glu Ile Ile
1 5 10 15

Arg Ile Ser Lys Ala Gln Ser Ile Arg Ile Lys Glu Leu Gln Leu Glu
20 25 30

Asn Glu Arg Leu Leu Ser Glu Asn Ile Asp Leu Arg Thr
35 40 45

<210> 23
<211> 45
<212> PRT
<213> yeast

<400> 23

Val Glu Asn Ile Arg Gln Ser Tyr Ser Arg Gln Asn Ser Leu Leu Ala
1 5 10 15

Lys Asp Asn Ser Ile Leu Lys Ile Lys Val Asn Ser Leu Glu Lys Lys
20 25 30

Ile Ser Gln Leu Val Gln Glu Asn Val Thr Leu Arg Ser
35 40 45

Substitute_Sequence_Listing.TXT

<210> 24
 <211> 45
 <212> PRT
 <213> Neurospora crassa

<400> 24

Leu Glu Leu Leu Arg Arg Lys Phe Leu Arg Gln Asn Arg Asp Ile Ala
 1 5 10 15

Arg Val Asn Ser Thr Gln Ser Leu Arg Ile Arg Gly Leu Glu Asn Glu
 20 25 30

Cys Ala Arg Leu Leu Ser Glu Asn Leu Glu Leu Arg Gly
 35 40 45

<210> 25
 <211> 45
 <212> PRT
 <213> Dactylicapnos macrocapnos

<400> 25

Gly Ser Lys Val Glu Gln Gln Tyr Lys Leu Leu Asn Ala Glu Leu Met
 1 5 10 15

Asp Gln Val Gln Lys Gln Arg Leu Glu Ile Gly Glu Tyr Arg Lys Arg
 20 25 30

Val Ile Ser Leu Glu Arg Glu Ile Met Asp Ile Arg Glu
 35 40 45

<210> 26
 <211> 27
 <212> PRT
 <213> yeast

<400> 26

Gly Arg Glu Lys Leu Arg Arg Ser Val Lys Val Ile Asn Tyr Ala Ile
 1 5 10 15

Pro Ser Leu Arg Thr Lys Leu Arg Arg Asp Phe
 20 25

<210> 27
 <211> 27
 <212> PRT
 <213> yeast

<400> 27

Pro Asp Gly Arg Ser Arg Arg Glu Arg Lys Lys Val Asn Tyr Ala Leu

Substitute_Sequence_Listing.TXT

1 5 10 15

Pro Gly Leu Arg Thr Lys Leu Arg Arg Asn Phe
20 25

<210> 28
<211> 28
<212> PRT
<213> yeast

<400> 28

Ser Phe Thr Arg Thr Arg Arg Thr Arg Gly Lys Ala Val Asp Tyr Thr
1 5 10 15

Leu Pro Ser Leu Arg Ala Lys Met Arg Arg Pro Ser
20 25

<210> 29
<211> 28
<212> PRT
<213> Neurospora crassa

<400> 29

Glu Thr Ser Arg Pro Ser Arg Arg Ala Arg Ala Ala Ile Ser Tyr Thr
1 5 10 15

Glu Pro Asn Leu Arg Asp Lys Met Arg Arg Pro Thr
20 25

<210> 30
<211> 27
<212> PRT
<213> Dactylicapnos macrocapnos

<400> 30

Asn Ser Ala Arg Pro Ser Arg Ser Cys Arg Pro Thr Ser Leu Val Glu
1 5 10 15

Pro Ser Leu Lys Asn Lys Leu Arg Asn Gly Ser
20 25

<210> 31
<211> 28
<212> PRT
<213> Caenorhabditis elegans

<400> 31

Thr Val Arg Arg Gln Arg Ser Ala Lys Met Asn Ile Lys Ser Leu Lys
1 5 10 15

Substitute_Sequence_Listing.TXT

Glu Pro Ser Gly Lys Asp Lys Leu Arg Arg Pro Gly
20 25

<210> 32
<211> 29
<212> PRT
<213> Arabidopsis thaliana

<400> 32

Thr Val Gly Arg Pro Ser Arg Gln Ala Ala Glu Lys Ile Lys Ser Tyr
1 5 10 15

Lys Glu Pro Ser Leu Lys Glu Lys Met Arg Gly Gly Phe
20 25

<210> 33
<211> 29
<212> PRT
<213> Arabidopsis thaliana

<400> 33

Ser Val Gly Arg Pro Ser Arg His Ala Ala Glu Lys Val Gln Ser Tyr
1 5 10 15

Arg Glu Val Ser Leu Arg Val Lys Met Arg Arg Lys Cys
20 25

<210> 34
<211> 28
<212> PRT
<213> mouse

<400> 34

Ala Val Ala Leu Thr Lys Arg Arg Cys Ser Thr Ile Lys Ser Tyr Lys
1 5 10 15

Glu Pro Thr Leu Ala Ser Lys Leu Arg Arg Gly Asp
20 25

<210> 35
<211> 25
<212> PRT
<213> mouse

<400> 35

His Pro Met Arg Arg Lys Arg Gln Cys Val Pro Leu Asn Leu Thr Glu
1 5 10 15

Pro Ser Leu Arg Ser Lys Met Arg Arg
20 25

Substitute_Sequence_Listing.TXT

<210> 36
 <211> 28
 <212> PRT
 <213> Homo sapiens

<400> 36

Ala Val Ala Leu Pro Lys Arg Arg Cys Thr Ala Ser Val Asn Tyr Lys
 1 5 10 15

Glu Pro Thr Leu Ala Ser Lys Leu Arg Arg Gly Asp
 20 25

<210> 37
 <211> 26
 <212> PRT
 <213> Homo sapiens

<400> 37

Ser Glu Arg Thr Ser Arg Arg Arg Arg Cys Thr Pro Phe Tyr Phe Lys
 1 5 10 15

Glu Pro Ser Leu Arg Asp Lys Met Arg Arg
 20 25

<210> 38
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ?Triplex

<400> 38
 ctcggaagc ggcattgt g 21

<210> 39
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 39
 cctggctgaa tcagcttgg tg 22

<210> 40
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> hSgo1

<400> 40
 aagucuacug auaugucuu att 23

<210> 41

Substitute_Sequence_Listing.TXT

```

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> hSgo2

<400> 41
aagcacuacc acuuugaaua att 23

<210> 42
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> hSgo1

<400> 42
gugagccucu gugaaucaat t 21

<210> 43
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> hSgo2

<400> 43
gcucucauga acaauaacut t 21

<210> 44
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA,Target1

<400> 44
gagugaucac gauuucuaat t 21

<210> 45
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA,Target2

<400> 45
aacgggcuu ugaauaugaa a 21

```

Substitute_Sequence_Listing.TXT